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80 61 2.4 982 17 AF011221 AF011221
81 61 2.4 1080 14 BM810567 AGENCOURT
82 61 2.4 1189 12 BG611991 BG611991
83 60 2.3 490 17 BH152886 BH152886
84 59 2.3 226 12 BF854329 BF854329
85 59 2.3 263 9 AA825185 AA825185
86 59 2.3 312 17 AF166285 AF166285
87 59 2.3 317 9 AA573000 AA573000
88 59 2.3 349 10 AW770050 AW770050
89 59 2.3 379 17 A0580711 A0580711
90 59 2.3 382 12 AA219031 AA219031
91 59 2.3 383 12 BF755195 BF755195
92 59 2.3 409 13 BG952898 BG952898
93 59 2.3 420 9 AA835931 AA835931
94 59 2.3 422 9 AA743968 AA743968
95 59 2.3 440 17 B17487 B17487
96 59 2.3 447 17 A0038575 A0038575
97 59 2.3 518 17 A0412294 A0412294
98 59 2.3 524 12 BF737749 BF737749
99 59 2.3 540 9 AL699257 AL699257
100 59 2.3 592 14 B0272418 B0272418

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ALIGNMENTS

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RESULT 1
AL541041 877 bp mRNA linear EST 16-FEB-2001
LOCUS AL541041 LTI FL002_PUL Homo sapiens CDNA clone CS0DB005YK23 5 prime
DEFINITION / mRNA sequence.
ACCESSION AL541041
VERSION AL541041.1 GI:12871733
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 877)
AUTHORS Li W.B., Gruber C., Jeesee J. and Polayes D.
TITLE Full-length CDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr.
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DB005YK23"
/clone_1b="LTI_FL002_PUL"
/lab_host="DH10B"
/notes="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
CDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded CDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
liang@life.com URL:
http://fulllength.invitrogen.com"
BASE COUNT 192 a 262 c 251 g 170 t 2 others
ORIGIN

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Query Match 30.3%; Score 778; DB 9; Length 877;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 29 CAAGAGCCCAAGCCTGTCTGTGTGACAGAGCTCAAGAGGCGCTGGGCTTCCCTCC 88
Db 1 CAAGAGCCCAAGCCTGTCTGTGTGACAGAGCTCAAGAGGCGCTGGGCTTCCCTCC 60

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QY 89 TGGCTCGGCTGTGTCTGTGGAGGGTTCCCACTCCAGAAATCCCTAAGGAGATGGGGCAGC 148
Db 61 TGGCTCGGCTGTGTCTGTGGAGGGTTCCCACTCCAGAAATCCCTAAGGAGATGGGGCAGC 120
QY 149 TGAATCAATCCCTGTGTGTCAAACTGTGACAGACAGATGTGAGCTTAACCAACCA 208
Db 121 TGAATCAATCCCTGTGTGTCAAACTGTGACAGACAGATGTGAGCTTAACCAACCA 180
QY 209 CACTCAATCCCTGTGTGTCAAACTGTGACAGACAGATGTGAGCTTAACCAACCA 268
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QY 269 AGGACACTGGGACACTTCCAGAGAGGCGCCCAAGCCCTTAACCTGTGACAGACAGATG 328
Db 241 AGGACACTGGGACACTTCCAGAGAGGCGCCCAAGCCCTTAACCTGTGACAGACAGATG 300
QY 329 GGTCTCAGCAGAGCTGTCTTCCCAAGCTTGTGATGACAAATTTTCCCTGATGATGT 388
Db 301 GGTCTCAGCAGAGCTGTCTTCCCAAGCTTGTGATGACAAATTTTCCCTGATGATGT 360
QY 389 GCTTCTGAGTGTCTGTGAGGAACTATGGAAGTCTGCCAGACAGAGAAATCTCTGC 448
Db 361 GCTTCTGAGTGTCTGTGAGGAACTATGGAAGTCTGCCAGACAGAGAAATCTCTGC 420
QY 449 CAAGCCCAAGCTTGAATCTCTGTCCAAAGCCAGAGACCTGTGACATGAGAGAGAGAG 508
Db 421 CAAGCCCAAGCTTGAATCTCTGTCCAAAGCCAGAGACCTGTGACATGAGAGAGAGAG 480
QY 509 GAAGCAAGGCAAGAGCGGTGCGCTGGGCAATTCCTCCGAGGTGGCCGCGAGCTGT 568
Db 481 GAAGCAAGGCAAGAGCGGTGCGCTGGGCAATTCCTCCGAGGTGGCCGCGAGCTGT 540
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Db 601 TGTCTGAAGTCTCAGGACAGAGATTAACATCCCAAGCGTCAAGTGGCCAAAGTCTCC 660
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QY 749 GGAACCTGAGAGGAGGCTTCTCATCCGGAGAGGAGAGAGAGAGAGAGAGAGAGAG 808
Db 721 GGAACCTGAGAGGAGGCTTCTCATCCGGAGAGGAGAGAGAGAGAGAGAGAGAGAG 780
QY 809 TGTCTGATCCGCTCAGAGCGCTGATCCGTGGAGACCGATCAGACACTA 857
Db 781 TGTCTGATCCGCTCAGAGCGCTGATCCGTGGAGACCGATCAGACACTA 829

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RESULT 2
LOCUS B0052308 1002 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT_6868571 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:593542
LOCUS B0052308 5', mRNA sequence.
ACCESSION B0052308
VERSION B0052308.1 GI:19811648
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1002)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Straube, Ph.D.
Email: cga@bbs-riemail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DMS/NCI

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CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNCM2118 row: d column: 23
 High quality sequence stop: 670.

FEATURES

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 /db_xref="taxon:9606"
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 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: blood; Vector: pORF7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC Library."

BASE COUNT 221 a 296 c 288 g 197 t
 ORIGIN

Query Match 27.2%; Score 698; DB 14; Length 1002;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 748; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 350 CCAAGCCTTGATGACAAACCAATTCCTCCGATGATGCTGTGAGTGGCTCTGAG 409
 Db 31 CCAAGCCTTGATGACAAACCAATTCCTCCGATGATGCTGTGAGTGGCTCTGAG 90
 QY 410 GACCAATGGGAGTCTGCCACGAGAAATTCCTCCGAGCCCAAGCTTGAATCTT 469
 Db 91 GACCAATGGGAGTCTGCCACGAGAAATTCCTCCGAGCCCAAGCTTGAATCTT 150
 QY 470 CTGTCCAAAGCCAGGAGCCTGTGACATGTGAGAGAGAGAGAGAGAGAGAGAG 529
 Db 151 CTGTCCAAAGCCAGGAGCCTGTGACATGTGAGAGAGAGAGAGAGAGAGAGAG 210
 QY 530 CCTGGGAGATTTCCCGGAGGTGGCCCGGCGAGCTGTCTGTAGAGCTCGGGAG 589
 Db 211 CCTGGGAGATTTCCCGGAGGTGGCCCGGCGAGCTGTCTGTAGAGCTCGGGAG 270
 QY 590 TGACCATGCTCTGTGAGAGTGAAGAGTGTGAGAGTGTGAGAGTGTGAGAGAG 649
 Db 271 TGACCATGCTCTGTGAGAGTGAAGAGTGTGAGAGTGTGAGAGTGTGAGAG 330
 QY 650 AGTATTAACATCCCAAGCTTCAAGTGTGAGAGTGTGAGAGTGTGAGAGAG 709
 Db 331 AGTATTAACATCCCAAGCTTCAAGTGTGAGAGTGTGAGAGTGTGAGAGAG 390
 QY 710 TGACAGAGAGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 769
 Db 391 TGACAGAGAGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 450
 QY 770 TCATTCGGGAGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 829
 Db 451 TCATTCGGGAGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 510
 QY 830 CTGCAATCTGGAGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAG 889
 Db 511 CTGCAATCTGGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 570
 QY 890 ACATCTCAACGGGCTCACTTCCCTCACTCAAGGCTGTGAGAGAGAGAGAGAG 949
 Db 571 ACATCTCAACGGGCTCACTTCCCTCACTCAAGGCTGTGAGAGAGAGAGAGAG 630
 QY 950 TGGGAGATGATCTGCTGCTACTCAAGAGAGCCCTGTGTCTCAAGAGAGAGAG 1009

Db 631 TGGGAGATGATCTGCTGCTACTCAAGAGAGCCCTGTGTCTCAAGAGAGAGAG 690
 QY 1010 TCCCTGGCAAGAGATATACCCCTAAGTGTGAGAGAGAGAGAGAGAGAGAG 1069
 Db 691 TCCCTGGCAAGAGATATACCCCTAAGTGTGAGAGAGAGAGAGAGAGAGAGAG 750
 QY 1070 AGCTGAGAGAGTCCCTGCTGTTTCTGAA 1098
 Db 751 AGCTGAGAGAGTCCCTGCTGTTTCTGAA 779

RESULT 3
 B677567
 LOCUS
 DEFINITION 794 bp mRNA linear EST 01-MAY-2001
 602624118P1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748884 5',
 mRNA sequence.
 B677567
 B677567.1 GI:13908964
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 794)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@b6-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: InCyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM10601 row: d column: 05
 High quality sequence stop: 790.

FEATURES

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1..794
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 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 192 a 229 c 212 g 161 t
 ORIGIN

Query Match 24.6%; Score 631; DB 12; Length 794;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 946 GAGTGGCCGATGATGATGCTGTGCTCAAGAGAGCCCTGTGTCTGTGAGAGAGAG 1005
 Db 17 GAGTGGCCGATGATGATGCTGTGCTCAAGAGAGCCCTGTGTCTGTGAGAGAGAG 76
 QY 1006 CCGTCCCTGGCAAGATATACCCCTACTGTGACTGTGAGAGAGAGAGAGAGAG 1065
 Db 77 CCGTCCCTGGCAAGATATACCCCTACTGTGACTGTGAGAGAGAGAGAGAGAG 136
 QY 1066 AAAGAGCTGAGAGAGTCCCTCTGTTTGTGAAGTGTGAGAGAGAGAGAGAG 1125
 Db 137 AAAGAGCTGAGAGAGTCCCTCTGTTTGTGAAGTGTGAGAGAGAGAGAGAGAG 196
 QY 1126 AGTGAAGGCTCTCGGAGAGTCCCTCACTTCAATCAAGCTGATGAGAGAGAG 1185
 Db 197 AGTGAAGGCTCTCGGAGAGTCCCTCACTTCAATCAAGCTGATGAGAGAGAGAG 256

Qy	1186	TTGATGATCCCTAGAGCCCAAGAGAGGCCAAGAGGAAACAAGGCTGACACCTGAA	1245
Db	257	TTGATGATGCTTAAGGCCCAAGAGAGGCCAAGAGGAAACAAAGGCTGACACCTGAA	316
Qy	1246	ACCCCAATTAGGCTCTCTGGGCAACCCCAAGCAAGGCTGTGACTCAGGAGAGGAGGCT	1305
Db	317	ACCCCAATTAGGCTCTCTGGGCAACCCCAAGCAAGGCTGTGACTCAGGAGAGGAGGCT	376
Qy	1306	GGGACACAGAGGTGCATCTAGAGGTCCCACTGTACCTTGTCTCTTTCTCTCTTAAAGCCT	1365
Db	377	GGGACACAGAGGTGCATCTAGAGGTCCCACTGTACCTTGTCTCTTTCTCTCTTAAAGCCT	436
Qy	1366	TGAGAGTGAACCTACTTCCCTCAGTGTGCATGTATCCACCTGGAGACTCTATGTCCAGATGC	1425
Db	437	TGAGAGTGAACCTACTTCCCTCAGTGTGCATGTATCCACCTGGAGACTCTATGTCCAGATGC	496
Qy	1426	AAGAGAAAGTGGGACACAGGGCCAGGGTTCCAAAAAGAGATTAAGCTCTGTGGGGGATCTGAA	1485
Db	497	AAGAGAAAGTGGGACACAGGGCCAGGGTTCCAAAAAGAGATTAAGCTCTGTGGGGGATCTGAA	556
Qy	1486	CCTAATTAGTTCTTTGAGTTTGGGATTTCCAGTACCATCTGTGAATGCCCTGTGAGACT	1545
Db	557	CCTAATTAGTTCTTTGAGTTTGGGATTTCCAGTACCATCTGTGAATGCCCTGTGAGACT	616
Qy	1546	CCATTCTACATCCCAACATTAACAGAGGCC	1576
Db	617	CCATTCTACATCCCAACATTAACAGAGGCC	647

RESULT 4	BO054265	986 bp	mRNA	linear	EST: 29-MAR-2002
LOCUS	BO054265				
DEFINITION	AGGCCGCTTGC830248 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:53563353				
ACCESSION	BO054265				
VERSION	BO054265.1	GI:19813605			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE
(bases 1 to 986)
AUTHORS
NIH-MGC <http://imgc.nhl.nih.gov/>
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Dr. Daniel McVicar, DSB/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MSC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LNC2125 row: 1 column: 12
High quality sequence strip: 515.

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/clone="IMAGE:5936339"
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/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: blood; Vector: pOTB1; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG (g). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NH_MGC Library."
BASE COUNT
211 a 291 c 276 g 207 t 1 others

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ORIGIN

Query Match	24.5%	Score 629	DB 14	Length 986
Best Local Similarity	100.0%	Prod. No. 0		
Matches 629	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy	137	GGATGGGGGACGGTATTCATTCCGTGGTGA	CAAACTGCTGA	CTGCA	CAAGATGCTGAGC	136
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Oy	197	TACCCAAACCAACCTTAGCCTCTCCCTGA	AGATCTCC	CACGGCTGAGAGATTCCTGGT		256
Db	61	TACCCAAACCAACCTTAGCCTCTCCCTGA	AGATCTCC	CACGGCTGAGAGATTCCTGGT		120
Oy	257	GTCTTAGAGCAACAAGACACTGGAGAC	ATTCAGAGGGGCC	CCCCAAGCCTTAACCTGTCC		316
Db	121	GTCTTAGAGCAACAAGACACTGGAGAC	ATTCAGAGGGGCC	CCCCAAGCCTTAACCTGTCC		180
Oy	317	AGCCAGACATGGCGTCTGAGAGAGCTGTCTCC	AGGCGTTGATGA	CAACCAATTC		376
Db	181	AGCCAGACATGGCGTCTGAGAGAGCTGTCTCC	AGGCGTTGATGA	CAACCAATTC		240
Oy	377	CCTCGATGATGTGCTTCTGATGCTCTGCTG	AGAA	CAATGGAGATCTGCCACAGAA		436
Db	241	CCTCGATGATGTGCTTCTGATGCTCTGCTG	AGAA	CAATGGAGATCTGCCACAGAA		300
Oy	437	GAATAATCTCTGGCAAGCCCAAGCTTGA	AGTTGATCTCTG	CCCAAGCCAGAGAC	CTGTGACA	496
Db	301	GAATAATCTCTGGCAAGCCCAAGCTTGA	AGTTGATCTCTG	CCCAAGCCAGAGAC	CTGTGACA	360
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Oy	557	CGGCGACGATGTGCTGAGATCGGAGAG	ACATTGACATCGTCTCTG	AGATGAGACT		616
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Db	481	GGTGAAGGTGTGCTGTCTGAAGCTCAGGG	CAGAGATTAACATCCCCAGGTCTCAGTGG			540
Oy	677	CCAAAGCTCCCATGGGTGCTTATGAGGGC	CTGAGCAAGGAGAAAGCAGAGAACTGC			736
Db	541	CCAAAGCTCCCATGGGTGCTTATGAGGGC	CTGAGCAAGGAGAAAGCAGAGAACTGC			600
Oy	737	TTGTGTACTCTGGGAA	CCCTGAGAGGGGCC			765
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LOCUS	
DEFINITION	B0054281 1020 bp mRNA linear EST 29-MAR-2002
ACCESSION	AGNCOUNT 6830234 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936367
VERSION	5', mRNA sequence.
KEYWORDS	B0054281 GI:19813621
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1020) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Robert Strausberg, Ph.D.
TITLE	Email: cgepbbs-remail.nih.gov
JOURNAL	Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
COMMENT	CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULML) DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov

Plate: LNCM2125 row: j column: 11
High quality sequence stop: 556.

FEATURES

Location/Qualifiers

1..1020

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/note="Organ: blood; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 219 a 311 c 283 g 204 t 3 others

ORIGIN

Query Match 24.1%; Score 619; DB 14; Length 1020;
Best Local Similarity 99.7%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;
Matches 719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

208 ACACCTAGCCTCTCCCTGAGAGCTCTCCAGGCTGAGAGATTGCTGCTAGAGACC 267
5 ACACCTAGCCTCTCCCTGAGAGCTCTCCAGGCTGAGAGATTGCTGCTAGAGACC 64
268 AAGGACACTGCGAGACTTCCAGAGAGGCCCCCAAGCCCTAACCTGACGACAGAT 327
65 AAGGACACTGCGAGACTTCCAGAGAGGCCCCCAAGCCCTAACCTGACGACAGAT 124
328 GCGTCTGAGAGAGCTGCTTCCCAAGCCTTTGATGACAAACCAATTTCTCGATGATG 387
125 GCGTCTGAGAGAGCTGCTTCCCAAGCCTTTGATGACAAACCAATTTCTCGATGATG 184
388 TGCTTGTGAGTGTCTGCTGAGAGCAATGGAGTGTGCGCAGAGAGAAATCTCTG 447
185 TGCTTGTGAGTGTCTGCTGAGAGCAATGGAGTGTGCGCAGAGAGAAATCTCTG 244
448 CCAAGCCCAAGCTTGAATCTCTGCTGCAAGGCGGAGCCTGTGACATGAGACAGAG 507
245 CCAAGCCCAAGCTTGAATCTCTGCTGCAAGGCGGAGCCTGTGACATGAGACAGAG 304
508 AGAAGCAAGGCGCAGAGCCTGAGGAGGAGTTCGCGAGAGTGGCCCGGCGAGAGTG 567
305 AGAAGCAAGGCGCAGAGCCTGAGGAGGAGTTCGCGAGAGTGGCCCGGCGAGAGTG 364
568 TGCGTGAAGTGGGAGGCAATGACATGCTCTGAGAGTGAAGATGATGACGAGTG 627
365 TGCGTGAAGTGGGAGGCAATGACATGCTCTGAGAGTGAAGATGATGACGAGTG 424
628 CTGCTGAAGTCTCAGGAGAGAGTAAATATCCACGCTGCAAGGCGCAAGTCTTC 687
425 CTGCTGAAGTCTCAGGAGAGAGTAAATATCCACGCTGCAAGGCGCAAGTCTTC 484
688 CATGGTGGCTGATGAGAGGCTGAGAGAGGAGAAAGAGAGAACTGCTGTGTTA 747
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748 GGGAGCCCTGAGAGGAGGCTTCTCTCATCCGAGAGAGCAGAGAGAGGCTTACT 807
545 GNGAGCCCTGAGAGGAGGCTTCTCTCATCCGAGAGAGCAGAGAGAGGCTTACT 604
808 CTGCTGAAGTCTCAGGAGAGGCTTCTCTCATCCGAGAGAGCAGAGAGAGGCTTACT 867
605 CTGCTGAAGTCTCAGGAGAGGCTTCTCTCATCCGAGAGAGCAGAGAGAGGCTTACT 664
868 TGCGTGAAGTGGGAGGCAATGACATGCTCTGAGAGTGAAGATGATGACGAGTG 927

Db 665 TGCTTGAAGTGGGAGGCAATGACATGCTCTGAGAGTGAAGATGATGACGAGTG 124
Qy 928 C 928
Db 725 C 725

RESULT 6
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LOCUS
DEFINITION
BQ052468 1069 bp mRNA linear EST 29-MAR-2002
AGENCOURT 6868422 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:5933772
5', mRNA sequence.
ACCESSION
BQ052468
VERSION
BQ052468.1 GI:19811808
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1069)
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
CONTACT
Contact: Robert Strausberg, Ph.D.
Email: cgsdp@remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DMS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM2118 row: n column: 13
High quality sequence stop: 681.

FEATURES

source

1..1069

Location/Qualifiers

/organism="Homo sapiens"
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/issue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 230 a 328 c 300 g 205 t 6 others

ORIGIN

Query Match 23.6%; Score 605; DB 14; Length 1069;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

327 TGCGTTCAGAGAGCTGCTTCCCAAGCCTTTGATGACAAACCAATTTCTCGATGAT 386
Db 1 TGCGTTCAGAGAGCTGCTTCCCAAGCCTTTGATGACAAACCAATTTCTCGATGAT 60
Qy 387 GTGCTTGAAGTGTCTGCTGAGAGAAATGGAAGTGTGCCAGAGAGAAATCTCT 446
Db 61 GTGCTTGAAGTGTCTGCTGAGAGAAATGGAAGTGTGCCAGAGAGAAATCTCT 120
Qy 447 GCCAAGCCCAAGCTTGAATCTCTGCTGCAAGGCGGAGAGCCTGTGACATGAGAGAG 506
Db 121 GCCAAGCCCAAGCTTGAATCTCTGCTGCAAGGCGGAGAGCCTGTGACATGAGAGAG 180
Qy 507 GAGAAGCAAGGCGCAGAGCCTGAGGAGGAGTTCGCGAGAGTGGCCCGGCGAGAGTG 566
Db 181 GAGAAGCAAGGCGCAGAGCCTGAGGAGGAGTTCGCGAGAGTGGCCCGGCGAGAGTG 240

QY 567 GTGCTGAGACTCGGGAGCATTGACCATGCTCTGAGAGTGGAGACTGGTGA CGGT 626
 |||||
 Db 241 GTGCTGAGACTCGGGAGCATTGACCATGCTCTGAGAGTGGAGACTGGTGA CGGT 300
 QY 627 GGTGCTGAACTCGAGGAGAGATTAATATCCACGCTCAAGGCTCAAAATCTC 686
 |||||
 Db 301 GGTGCTGAACTCGAGGAGAGATTAATATCCACGCTCAAGGCTCAAAATCTC 360
 QY 687 CCATGGGTGCTGATAGAGGCGCTGAGCAGGAGAAAGCAGAGAACTGCTGTTC 746
 |||||
 Db 361 CCATGGGTGCTGATAGAGGCGCTGAGCAGGAGAAAGCAGAGAACTGCTGTTC 420
 QY 747 TGGGAACCTGAGAGGCGCTTCCTCATCCGGAGAGCAGACAGAGAGAGGCTCTTAC 806
 |||||
 Db 421 TGGGAACCTGAGAGGCGCTTCCTCATCCGGAGAGCAGACAGAGAGAGGCTCTTAC 480
 QY 807 TCTGTCACTCCGCTCAGCGCGCTGCATCTGGGACCGGATCAGACATACAGATCCA 866
 |||||
 Db 481 TCTGTCACTCCGCTCAGCGCGCTGCATCTGGGACCGGATCAGACATACAGATCCA 540
 QY 867 CTGCTGACAACTGCTGCTGATACATCTCAGCGCGCTCAGCTTCCGCTCAGCTGAGG 926
 |||||
 Db 541 CTGCTGACAACTGCTGCTGATACATCTCAGCGCGCTCAGCTTCCGCTCAGCTGAGG 600
 QY 927 CCTGG 931
 |||||
 Db 601 CCTGG 605

RESULT 7
 AL568702/c 854 bp mRNA linear EST 16-FEB-2001
 LOCUS AL568702 LIT_Fl002_P11 Homo sapiens cDNA clone CS0DB005YK23 3 prime
 DEFINITION
 ' mRNA sequence.
 ACCESSION AL568702
 VERSION AL568702.1 GI:12923305
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 854)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Source
 1. 854
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DB005YK23"
 /clone_11b="LIT_Fl002_P11"
 /lab_host="DH10B"
 /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by Life
 Technologies. Contact : Feng Liang Life Technologies, a
 Division of Invitrogen 9800 Medical Center Drive Rockville
 Maryland 20850, USA Fax : (1) 301 610 8371 Email :
 fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 195 a 200 c 236 g 219 t 4 others
 ORIGIN

Query Match 23.4%; Score 600; DB 9; Length 854;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1841 TTTTGTGAGAGGAGTCTTGCCCTGTTGCCATCTGGAAGTGAATGGCAGATCTCAG 1300
 |||||
 Db 602 TTTTGTGAGAGGAGTCTTGCCCTGTTGCCATCTGGAAGTGAATGGCAGATCTCAG 543
 QY 1901 CTCACCTGCAACCTCCATCTCTGGAATCAAAATTCCTGCTGAGCTCCAGATAG 1960
 |||||
 Db 542 CTCACCTGCAACCTCCATCTCTGGAATCAAAATTCCTGCTGAGCTCCAGATAG 483
 QY 1961 CTGGGATTTACAGGCGTACACACATGCTGCTGTAATTTTGTATTTTGTATGAT 2020
 |||||
 Db 482 CTGGGATTTACAGGCGTACACACATGCTGCTGTAATTTTGTATTTTGTATGAT 423
 QY 2021 GGGGTTTCAACATTTGGCAGGCTGATGCAATCCCTGACCTCAGGTGATCCAC 2080
 |||||
 Db 422 GGGGTTTCAACATTTGGCAGGCTGATGCAATCCCTGACCTCAGGTGATCCAC 363
 QY 2081 CTGGGCTCCCAAGTGTCTGGGATTTACAGGTGAGCCAGGACCCAGCTTCTCA 2140
 |||||
 Db 362 CTGGGCTCCCAAGTGTCTGGGATTTACAGGTGAGCCAGGACCCAGCTTCTCA 303
 QY 2141 GATCTATTTTCAATTTTGTGCTTACCATTTCCCTAGACA CACTGCGCTTGCATCTTGTG 2200
 |||||
 Db 302 GATCTATTTTCAATTTTGTGCTTACCATTTCCCTAGACA CACTGCGCTTGCATCTTGTG 243
 QY 2201 CCGAATTAATAAATAACACTCTTAAGCTTACGACACTGACAGGACGACGACTCAGT 2260
 |||||
 Db 242 CCGAATTAATAAATAACACTCTTAAGCTTACGACACTGACAGGACGACGACTCAGT 183
 QY 2261 GCTGGGAGGAGGATCAGAGGATCTAAGGCTCTCTCACAATGCCAGAGAGACCA 2320
 |||||
 Db 182 GCTGGGAGGAGGATCAGAGGATCTAAGGCTCTCTCACAATGCCAGAGAGACCA 123
 QY 2321 CAGCTTACCAATATCCAGCTTGAATTTCCCTGCTGCTCATAAAGAGAGAGGCT 2380
 |||||
 Db 122 CAGCTTACCAATATCCAGCTTGAATTTCCCTGCTGCTCATAAAGAGAGAGGCT 63
 QY 2381 GCTGGATCCGCTAAGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2440
 |||||
 Db 62 GCTGGATCCGCTAAGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3

RESULT 8
 AL844325 677 bp mRNA linear EST 30-JUL-2002
 LOCUS AL844325 pool_YT_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 AL844325
 ACCESSION AL844325
 VERSION AL844325.1 GI:22019105
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 677)
 AUTHORS Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J., and
 Sheridan, E.
 TITLE Homo sapiens EST sequence
 JOURNAL Unpublished (2002)
 COMMENT Contact: The Sanger Centre
 The Sanger Centre
 Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: humquery@sanger.ac.uk
 Sanger Centre name : scd10827.4004895
 Homo sapiens EST sequence. This sequence was generated as part of
 The Wellcome Trust Sanger Institute program to identify and
 annotate genes in the human genome. Incomplete or unconfirmed genes
 are experimentally analysed using a variety of cDNA library
 resources. This sequence was obtained from a PCR product generated
 from a pool of up to 100,000 cDNA clones derived from
 pool_YT_11b_v_SPD cDNA library. Further information can be found at
 http://www.sanger.ac.uk/Teams/Team69/.

FEATURES
 Source 1. 677
 Location/Qualifiers

OY 1625 CAGAAATCTACAGTCTGTTGAGACAC 1654
Db 30 CAGAAATCTACAGTCTGTTGAGACAC 1

RESULT 10
AL844308/c 642 bp mRNA linear EST 30-JUL-2002
LOCUS AL844308 pool_AK_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
DEFINITION AL844308
ACCESSION AL844308
VERSION AL844308.1 GI:22019090
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 642)
AUTHORS Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.
TITLE Homo sapiens EST sequence
JOURNAL Unpublished (2002)
COMMENT Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name: scd10816.400489A

Homo sapiens EST sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from pool_AK_11b_v_SPD cDNA library. Further information can be found at <http://www.sanger.ac.uk/teams/team9/>.

FEATURES

Location/Qualifiers
1..642

/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"

/clone_lib="pool_AK_11b_v_SPD"
/note="Organ: breast; Vector: pZero-1; Site 1: SphI; Site 2: SphI; Ductal carcinoma in situ, high-grade, comedo, from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
BASE COUNT 140 a 164 c 181 g 157 t

ORIGIN

Query Match 20.1%; Score 515; DB 9; Length 642;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1085 TCTGTTTTCTGAACTGCGACAGGGAGAGATCTTCTGACTGAGGCTCCGGAGT 1144
Db 588 TCTGTTTTCTGAACTGCGACAGGGAGAGATCTTCTGACTGAGGCTCCGGAGT 529

OY 1145 CCTCAGCTTCTACATCAGCTGAATGACGAGCGCTCTTGTGATGATCTAGGCC 1204
Db 528 CCTCAGCTTCTACATCAGCTGAATGACGAGCGCTCTTGTGATGATGCTAGGCC 469

OY 1205 AAGGAGAGGCAAAAGGAAACCAAGGCTGACACTAGAACCCCAATTAGCTCTG 1264
Db 468 AAGGAGAGGCAAAAGGAAACCAAGGCTGACACTAGAACCCCAATTAGCTCTG 409

OY 1265 GGACCCCGAGAGCAAGGCTGTGCACTCAGGAGAGGAGGTGGACACAGAGTGATCT 1324
Db 408 GGACCCCGAGAGCAAGGCTGTGCACTCAGGAGAGGAGGTGGACACAGAGTGATCT 349

OY 1325 AGGGTCCACCTGTAACCTTCTCTTCTTTAGCCTTGAAGTCACTTCTCT 1384
Db 348 AGGGTCCACCTGTAACCTTCTCTTCTTTAGCCTTGAAGTCACTTCTCTCT 289

OY 1385 TCCAGTGCATGATCCCACTGCGACCTGTAGTGAAGTCAAGAGAGTGGACAGG 1444

Db 288 TCCAGTGCATGATCCCACTGCGACCTGTAGTGAAGTGGACAGG 229
OY 1445 CCAGGTTCCAAAGAGATTAAGCTCTGAGGAGTCTGACCTAGTACTTCTGATT 1504
Db 228 CCAGGTTCCAAAGAGATTAAGCTCTGAGGAGTCTGACCTAGTACTTCTGATT 169
OY 1505 TGGGTTTCCAGTACATGATGAGGCTGCTGAGACCCCAATTACATCCACCA 1564
Db 168 TGGGTTTCCAGTACATGATGAGGCTGCTGAGACCCCAATTACATCCACCA 109

OY 1565 TTACACAGCCCAACCCACACAGTGAAGAACCC 1599
Db 108 TTACACAGCCCAACCCACACAGTGAAGAACCC 74

RESULT 11
AL844326/c 599 bp mRNA linear EST 30-JUL-2002
LOCUS AL844326 pool_YT_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
DEFINITION AL844326
ACCESSION AL844326
VERSION AL844326.1 GI:22019106
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 599)
AUTHORS Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.
TITLE Homo sapiens EST sequence
JOURNAL Unpublished (2002)
COMMENT Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name: scd10827.d1

Homo sapiens EST sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from pool_YT_11b_v_SPD cDNA library. Further information can be found at <http://www.sanger.ac.uk/teams/team9/>.

FEATURES

Location/Qualifiers
1..599

/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"

/clone_lib="pool_YT_11b_v_SPD"
/note="Organ: breast; Vector: pZero-1; Site 1: SphI; Site 2: SphI; Ductal carcinoma in situ, high-grade, comedo, from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
BASE COUNT 142 a 148 c 165 g 144 t

ORIGIN

Query Match 20.0%; Score 513; DB 9; Length 599;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1994 TAATTTTGTATTTTGTATGATGGGTTTACACATGGCAGAGCTGTGTGA 2053
Db 520 TAATTTTGTATTTTGTATGATGGGTTTACACATGGCAGAGCTGTGTGA 461

OY 2054 ACTCTGACCTCAGGATGATCCACCTTGGCTCCAAAGCTGAGTACAGGT 2113
Db 460 ACTCTGACCTCAGGATGATCCACCTTGGCTCCAAAGCTGAGTACAGGT 401

OY 2114 GAGCCAGGACCCAGCCTGATCTGATCTATTTATTTGTGCTTACATCC 2173
Db 400 GAGCCAGGACCCAGCCTGATCTGATCTATTTATTTGTGCTTACATCC 341

QY 2174 TAGCAGCTGGCTTGGCCATTTTGTGGCCGAATATAACCTTTAAGCTTACGA 2233
 DB 340 TAGCAGCTGGCTTGGCCATTTTGTGGCCGAATATAACCTTTAAGCTTACGA 281
 QY 2234 CACTGACGTGAGGCGAGGACCTGAGTGTGGGCGGGGAGTCAAGAGGTGCTAAGACCT 2233
 DB 280 CACTGACGTGAGGCGAGGACCTGAGTGTGGGCGGGGAGTCAAGAGGTGCTAAGACCT 221
 QY 2234 CTCTCCCAATGCGAAGACGAGACCAAGCTTACCAATTCAGCCCTTGAATTTCCCT 2353
 DB 220 CTCTCCCAATGCGAAGACGAGACCAAGCTTACCAATTCAGCCCTTGAATTTCCCT 161
 QY 2234 GCTGCTCCATTAACGAAAGAGGTGTGTGTGATCCGCTAAGGGATGAGGAGAGGA 2413
 DB 160 GCTGCTCCATTAACGAAAGAGGTGTGTGTGATCCGCTAAGGGATGAGGAGAGGA 101
 QY 2414 AAGAGGATGGGGTGGGAGGACCCCTCCAGTGTCTTACTGTTCCCAAGCTACAGT 2473
 DB 100 AAGAGGATGGGGTGGGAGGACCCCTCCAGTGTCTTACTGTTCCCAAGCTACAGT 41
 QY 2474 GGGGTGGAAAGGCTTTATCAGGTATCATCAAC 2506
 DB 40 GGGGTGGAAAGGCTTTATCAGGTATCATCAAC 8

RESULT 12
 BG284179 566 bp mRNA linear EST 21-FEB-2001
 LOCUS 602408226F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4520382 5'
 DEFINITION mRNA sequence.
 ACCESSION BG284179
 VERSION BG284179.1 GI:13034866
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 566)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LAM10418 row: c column: 07
 High quality sequence start: 2
 High quality sequence stop: 566.

FEATURES

Location/Qualifiers
 1..566
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4520382"
 /clone_id="NIH_MGC_91"
 /tissue_type="adenoecarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: PCMV-SPORT6, Site 1: NotI,
 Site 2: SalI; Cloned unidirectionally; oligo-dt primed.
 Average insert size 1.4 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH-MGC Library."
 BASE COUNT 116 a 187 c 152 g 110 t 1 others
 ORIGIN

Query Match 19.0%; Score 488; DB 12; Length 566;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 796 GGCTTTACTCTGTGTGATGCCCTCAGCGCCCTGCATCTGGAGCGGATCAGAC 855
 DB 13 GGCTTTACTCTGTGTGATGCCCTCAGCGCCCTGCATCTGGAGCGGATCAGAC 72
 QY 856 TACAGGATCAATGCTTGAACATGGCTGGCTGATCACTCACCGGCTTACCTTCCC 915
 DB 73 TACAGGATCAATGCTTGAACATGGCTGGCTGATCACTCACCGGCTTACCTTCCC 132
 QY 916 TCACTCAGGCTTGTGTGACATTACTCTGAGCTGGAGATGATCTGCTTACTC 975
 DB 133 TCACTCAGGCTTGTGTGACATTACTCTGAGCTGGAGATGATCTGCTTACTC 192
 QY 976 AAGGAGCCCTGTGTGCTGAGAGGAGGCTGCTCCCTGGGCAAGATATACCTTACT 1035
 DB 193 AAGGAGCCCTGTGTGCTGAGAGGAGGCTGCTCCCTGGGCAAGATATACCTTACT 252
 QY 1036 GTGACTGTGACAGGACACCACTCACTGGAAGAGCTGACAGTCCCTGTTTCT 1095
 DB 253 GTGACTGTGACAGGACACCACTCACTGGAAGAGCTGACAGTCCCTGTTTCT 312
 QY 1096 GAAGCTGCCAGAGGAGGAGGCTCTTCTCAGTGAAGGCTCCGGAGATCCCTGAGCTTC 1155
 DB 313 GAAGCTGCCAGAGGAGGAGGCTCTTCTCAGTGAAGGCTCCGGAGATCCCTGAGCTTC 372
 QY 1156 TACATCAGCTGATGACGAGGCTGTCTTGTGATGATCCTAGGCCCAAGAGAGGC 1215
 DB 373 TACATCAGCTGATGACGAGGCTGTCTTGTGATGATCCTAGGCCCAAGAGAGGC 432
 QY 1216 CAAAGAGGAACCAAGGCTGACACCTTGAAGCCCAATTTAGCTTCTGGGACCCAG 1275
 DB 433 CAAAGAGGAACCAAGGCTGACACCTTGAAGCCCAATTTAGCTTCTGGGACCCAG 492
 QY 1276 GGCAGAGC 1283
 DB 493 GGCAGAGC 500

RESULT 13

AL844311 597 bp mRNA linear EST 30-JUL-2002
 LOCUS AL844311 pool_YT_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION AL844311
 VERSION AL844311.1 GI:22019093
 KEYWORDS EST.

SOURCE

human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 597)
 Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
 Sheridan, E.

AUTHORS

Homo sapiens EST sequence
 Unpublished (2002)
 Contact: The Sanger Centre

TITLE

The Sanger Centre

JOURNAL

The Sanger Centre

COMMENT

The Sanger Centre

FEATURES

Location/Qualifiers
 1..597
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="20"
 /clone_id="pool_YT_11b_v_SPD"
 /note="Organ: breast; Vector: pZERO-1; Site 1: SphI;
 http://www.sanger.ac.uk/Teams/Team97/.

Query Match 19.0%; Score 488; DB 12; Length 566;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AUTHORS

Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.
Homo sapiens EST sequence
Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humgeny@sanger.ac.uk
Sanger Centre name: acc010817.400489A

FEATURES

source

Location/Qualifiers
1. 611
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_1b="pool FLU 11b v. SPC"
/note="Organ: breast; Vector: pZeo-1; Site: 1: SpH1;
Site 2: SpH1; Ductal carcinoma in situ, high-grade, comedo
from 41 yo female. Library constructed in the laboratory
of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
BASE COUNT 132 a 157 c 173 g 149 t

BASE COUNT

132 a 157 c 173 g 149 t

17.7%; Score 454; DB 9; Length 611;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match

Best Local Similarity 99.8%; Pred. No. 0;
Matches 504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1095 TGAAGCTGCACAGGAGGAGAGCTCTTCTCAATGAGGCTCTCCGAGTCCCTCACTT 1154
DB 577 TGAAGCTGCACAGGAGGAGAGCTCTTCTCAATGAGGCTCTCCGAGTCCCTCACTT 518
QY 1155 CTACATGAGCTGTAATGACGAGGCTGTCTTTGATGATGCTAGGCCCAAGAGAGG 1214
DB 517 CTACATGAGCTGTAATGACGAGGCTGTCTTTGATGATGCTAGGCCCAAGAGAGG 458
QY 1215 CCAAGAGGAAACCAAGGCTGCACACTGAAACCCCAATTAGCTTCTGGGACCCGAG 1274
DB 457 CCAAGAGGAAACCAAGGCTGCACACTGAAACCCCAATTAGCTTCTGGGACCCGAG 398
QY 1275 AGGCAAGGCTGTGCACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1334
DB 397 AGGCAAGGCTGTGCACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 338
QY 1335 CTGACCTTGTCTTCTTCTCTTAACTTAAAGTCACTTCTTCTTCAAGTCCA 1394
DB 337 CTGACCTTGTCTTCTTCTCTTAACTTAAAGTCACTTCTTCTTCAAGTCCA 278
QY 1395 TGATCCACCTGCGACCTCTAGTGCAGAGTGCAGAGAGGAGGAGGAGGAGG 1454
DB 277 TGATCCACCTGCGACCTCTAGTGCAGAGTGCAGAGAGGAGGAGGAGGAGG 218
QY 1455 AAAAAGAGAAATAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1514
DB 217 AAAAAGAGAAATAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 158
QY 1515 AGTACATCTGATGAGCTCTGCTTGTAGAGCCCATTTCAATCCCAATTAAACAGG 1574
DB 157 AGTACATCTGATGAGCTCTGCTTGTAGAGCCCATTTCAATCCCAATTAAACAGG 98
QY 1575 CCAAGCCCAAGGTAAGAAACAGCC 1599
DB 97 CCAAGCCCAAGGTAAGAAACAGCC 73

RESULT 16

BF510664/c

LOCUS

BF510664 451 bp mRNA linear EST 06-DEC-2000

DEFINITION

UT-H-B14-ae-f-b-01-0-UI.61 NCI CGAP Sub8 Homo sapiens cDNA clone

ACCESSION

IMAGE:3084601.3, mRNA sequence.
BF510664
BF510664.1 GI:11593962

VERSION

EST.

KEYWORDS

human.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 451)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

AUTHORS

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

TITLE

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrp/image/image.html
Seq primer: M13 Forward
POLYA=yes.

FEATURES

source

Location/Qualifiers
1. 451
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3084601"
/clone_1b="NCI CGAP Sub8"
/lab_note="DH10B (Life Technologies)"
/note="Vector: pTZ19-Pac (Pharmacia) with a modified
polylinker; Site: 1: Not 1; Site 2: Eco RI; NCI CGAP Sub8
is a subcloned library derived from NCI CGAP Sub5. The
NCI CGAP Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub5 was used
as a tracer in a subtractive hybridization with a driver
comprising: a pool of clones from NCI CGAP Sub5 (IMAGE
clone ids 2732833-2737415, 3068040-3069191, 25% of the
driver population), a pool of clones from NCI CGAP Sub4
(IMAGE clone ids 273592-2729326; 25% of the driver
population), NCI CGAP Sub6 (pool AIF-AJU, IMAGE ids
2728969-2733190; 25% of the driver population), and
NCI CGAP Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550
; 25% of the driver population). Subtraction was
performed as previously described [Bonaldi, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches to Facilitate Gene Discovery. Genome Research
6, 791-806.
TAG LIB=NCI CGAP Co10
TAG TISSUE=colon
TAG SRO=AAACG"

BASE COUNT

97 a 110 c 115 g 129 t

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2121 GGCACCAACCTAGCTCTGATCTCTATTTGATTTGGTGGCTTACCTCTAGACCA 2180
DB 441 GGCACCAACCTAGCTCTGATCTCTATTTGATTTGGTGGCTTACCTCTAGACCA 382
QY 2181 CTGGCTTCCATCTTGTGGCCGAATATAAATTAACCTCTTAAGTCTAGACATGCA 2240
DB 381 CTGGCTTCCATCTTGTGGCCGAATATAAATTAACCTCTTAAGTCTAGACATGCA 322
QY 2241 GTAGGCCAGGACCTAGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2300
DB 321 GTAGGCCAGGACCTAGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 262

QY 2301 CATTGCCAAGACGAGACACAGCCTTACCAATCCAGCCCTTATTCCTGCTGCT 2360
 |||||
 Db 261 CATTGCCAAGACGAGACACAGCCTTACCAATCCAGCCCTTATTCCTGCTGCT 202
 |||||
 QY 2361 CATTAAAGAAAGAGTGTGTGATCCGCTAAGGATCAGAGGAGAAAGAGG 2420
 |||||
 Db 201 CATTAAAGAAAGAGTGTGTGATCCGCTAAGGATCAGAGGAGAAAGAGG 142
 |||||
 QY 2421 ATGGGGTGGAGGACCCCTCCAGTGTCTTACTGCTTCCAGCTACAGGTGGGGTGG 2480
 |||||
 Db 141 ATGGGGTGGAGGACCCCTCCAGTGTCTTACTGCTTCCAGCTACAGGTGGGGTGG 82
 |||||
 QY 2481 GAAAGCTTTATCAGATCATCAACAGCTTCAATTAAGATTTGATTTCAAGTA 2540
 |||||
 Db 81 GAAAGCTTTATCAGATCATCAACAGCTTCAATTAAGATTTGATTTCAAGTA 22
 |||||
 QY 2541 TGTGAAAAAAAAAAAAAAAA 2561
 |||||
 Db 21 TGTGAAAAAAAAAAAAAAAA 1
 |||||

RESULT 17
 BG178487 778 bp mRNA linear EST 06-FEB-2001
 LOCUS 602328305F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:442986 5'
 DEFINITION mRNA sequence.
 ACCESSION BG178487
 VERSION BG178487.1 GI:12685190
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 778)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: sgabds-remail.nih.gov
 Tissue Procurement: DCTD/DRP

CDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM0182 row: 1 column: 01
 High quality sequence stop: 657.
 Location/Qualifiers

FEATURES
 source
 1..778
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:442986"
 /clone_lib="NIH_MGC_91"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: pCMV-SPORTS; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.4 Kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."
 BASE COUNT 179 a 224 c 230 g 145 t
 ORIGIN

Query Match 17.0%; Score 436; DB 12; Length 778;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 606; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 79 CTTCCTCTCTGCTGCTGCTGTGTGGAGGTTTCCCAAGTCCCAAGTCCCTAAGGAGC 138
 |||||
 Db 26 CTTCCTCTCTGCTGCTGCTGTGTGGAGGTTTCCCAAGTCCCAAGTCCCTAAGGAGC 85
 |||||
 QY 139 ATGGGCAAGCTGATCCATCCCTGTGTCAAACTGTAAGTGAAGACAGATCTGAGGCTA 198
 |||||

Db 86 ATGGGCAAGCTGATCCATCCCTGTGTGACAAATCTGTACAGACAGATCTAGCTA 145
 |||||
 QY 199 CCACAAACACACCTTACCTCTCCCTGAAGATCTCCAGGCTGAGAGATTTCTGGGTGT 258
 |||||
 Db 146 CCACAAACACACCTTACCTCTCCCTGAAGATCTCCAGGCTGAGAGATTTCTGGGTGT 205
 |||||
 QY 259 CCTAGACACAGGACATCTGCAATCTTCCAGAAAGGCCCCCAAGCCCTTACCTGTCCAG 318
 |||||
 Db 206 CCTAGACACAGGACATCTGCAATCTTCCAGAAAGGCCCCCAAGCCCTTACCTGTCCAG 265
 |||||
 QY 319 CCAGAGCATCGCTCAGCAGAGCTGTCTTCCCAAGCTTTGATGACAAACCAATTTCC 378
 |||||
 Db 266 CCAGAGCATCGCTCAGCAGAGCTGTCTTCCCAAGCTTTGATGACAAACCAATTTCC 325
 |||||
 QY 379 TCGATGATGTCTTCTGAGCTCTCTGTGAGAGAAAGGAGTGTGCGCCAGAGAGAA 438
 |||||
 Db 326 TCGATGATGTCTTCTGAGCTCTCTGTGAGAGAAAGGAGTGTGCGCCAGAGAGAA 385
 |||||
 QY 439 AAATCTCTGCCAAGCCCAAGCTTGAATTCCTCTGTCCAGGACCAGGACCTGTGACATG 498
 |||||
 Db 386 AAATCTCTGCCAAGCCCAAGCTTGAATTCCTCTGTCCAGGACCAGGACCTGTGACATG 444
 |||||
 QY 499 GAAAGACAGAGAAAGCAGAGCCACAGCCCTGCGCCCTGGGCAATTTCCCGAGTGGCCG 558
 |||||
 Db 445 GAAAGACAGAGAAAGCAGAGCCACAGCCCTGCGCCCTGGGCAATTTCCCGAGTGGCCG 504
 |||||
 QY 559 GCCGAGCTGTCTGCTGAGACTCGGGGAGCCATTTGACCATCTCTCTGAGATGAGACTGG 618
 |||||
 Db 505 GCCGAGCTGTCTGCTGAGACTCGGGGAGCCATTTGACCATCTCTCTGAGATGAGACTGG 564
 |||||
 QY 619 TGGACGCTGTCTGAGTCTGAGTCTCAGGACAGAGATTAATCATCCCAAGCCCTGAGCC 678
 |||||
 Db 565 TGGACGCTGTCTGAGTCTGAGTCTCAGGACAGAGATTAATCATCCCAAGCCCTGAGCC 624
 |||||
 QY 679 AAAGTCTC 686
 |||||
 Db 625 AAAGTCTC 632
 |||||

RESULT 18
 A1476149 409 bp mRNA linear EST 14-APR-1999
 LOCUS t162e12.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2174158 3'
 DEFINITION similar to contains element MER22 repetitive element ;, mRNA
 sequence.
 ACCESSION A1476149
 VERSION A1476149.1 GI:4329183
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 409)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: sgabds-remail.nih.gov
 Life Technologies catalog #: 11547-015
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert length: 2148 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 409.
 Location/Qualifiers

FEATURES
 source
 1..409
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2174158"

```

/clone_lib="NCI_CGAP_Lym12"
/tissue_type="Lymphoma, Follicular mixed small and large
cell"
/lab_host="DH10B"
/note="Organ: lymph node; Vector: pCMV-Sport6; Site: 1;
Sal1; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dr. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"

BASE COUNT      94 a      100 c      109 g      106 t

Query Match
Best Local Similarity 15.9%; Score 409; DB 9; Length 409;
Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2127 CAGCTAGCTCTCAGATCTCTATTCTTTGTGGCTTACCACTCCCTACACACTGGCC 2186
DB 409 CAGCTAGCTCTCAGATCTCTATTCTTTGTGGCTTACCACTCCCTACACACTGGCC 350
QY 2187 TTGCATCTTTGTGGCCGAATAAATAACACCTCTTAAGTCTAGCACTGCACTGAGG 2246
DB 349 TTGCATCTTTGTGGCCGAATAAATAACACCTCTTAAGTCTAGCACTGCACTGAGG 290
QY 2247 CCAGGACCTCTAGTGTGGGCGAGGGGATAGAAAGGTCTTAAGCCCTCTCCCAATGC 2306
DB 289 CCAAGCACTCTAGTGTGGGCGAGGGGATAGAAAGGTCTTAAGCCCTCTCCCAATGC 230
QY 2307 CAAAGCGAGACCAAGCTTACACCAATCCAGCCCTTGATTTCCCTGCTGCTCATTA 2366
DB 229 CAAAGCGAGACCAAGCTTACACCAATCCAGCCCTTGATTTCCCTGCTGCTCATTA 170
QY 2367 ACAGAAAGAGGTCTGTGGATCCGCTAAGGATCGAGGAGGAAAGGAAAGGAAATGGGG 2446
DB 169 ACAGAAAGAGGTCTGTGGATCCGCTAAGGATCGAGGAGGAAAGGAAAGGAAATGGGG 110
QY 2427 TGGAGGCAACCCCTCTCAAGTCTCTAAGTCTTCCCAAGCTACAGTGGGAGTGGAAAAG 2486
DB 109 TGGAGGCAACCCCTCTCAAGTCTCTAAGTCTTCCCAAGCTACAGTGGGAGTGGAAAAG 50
QY 2487 CTTATCAGGTATCATCAACAGGTTCTCAATTAAGATTATTTATTC 2535
DB 49 CTTATCAGGTATCATCAACAGGTTCTCAATTAAGATTATTTATTC 1

RESULT 19
BF057252/c 397 bp mRNA linear EST 16-OCT-2000
LOCUS 7K18A03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3444389 3',
DEFINITION mRNA sequence.
ACCESSION BF057252
VERSION BF057252.1 GI:10811148
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 397)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.lnl.gov
Seq primer: -40UP from Gibco.

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FEATURES
source Location/Qualifiers
1..397
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3444389"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
as circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones 18
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      88 a      100 c      100 g      109 t

Query Match
Best Local Similarity 15.5%; Score 397; DB 12; Length 397;
Pred. No. 0;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2154 TTTTGTGCTTACCAATCTCCCTAGACACTGCGCTTGTGCTTGTGGCGAATAAATAAT 2213
DB 397 TTTTGTGCTTACCAATCTCCCTAGACACTGCGCTTGTGCTTGTGGCGAATAAATAAT 338
QY 2214 AACACCTCTTAAGTCTAGCACTGCGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 2273
DB 337 AACACCTCTTAAGTCTAGCACTGCGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 278
QY 2274 ATCAGAAAGTGTAAAGCCCTCTCTCCCAATGCTCAAGCGAGACCAAGCTTACACCAA 2333
DB 277 ATCAGAAAGTGTAAAGCCCTCTCTCCCAATGCTCAAGCGAGACCAAGCTTACACCAA 218
QY 2334 ATCCAGCCCTTATTTCCCTGCTGCTCCATTAACAGAAAGAGTGTGTGGATCCGCTA 2293
DB 217 ATCCAGCCCTTATTTCCCTGCTGCTCCATTAACAGAAAGAGTGTGTGGATCCGCTA 158
QY 2394 AGGATCAGGAGAGAGAAAGAGGAGTGGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2453
DB 157 AGGATCAGGAGAGAGAAAGAGGAGTGGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 98
QY 2454 CTGGTCCCAAGCTTCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2513
DB 97 CTGGTCCCAAGCTTCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 38
QY 2514 CAATTAAAGATTGATTATTCAAGTATGTGAAAAA 2550
DB 37 CAATTAAAGATTGATTATTCAAGTATGTGAAAAA 1

RESULT 20
BF062179/c 397 bp mRNA linear EST 16-OCT-2000
LOCUS 7K73E03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3481060 3',
DEFINITION mRNA sequence.
ACCESSION BF062179
VERSION BF062179.1 GI:10821089
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 397)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

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Qy 2514 CAATTAAAGATTGATTATTCAGATGTAAGAAAA 2550
Db 37 CAATTAAAGATTGATTATTCAGATGTAAGAAAA 1

RESULT 24

BG255445

LOCUS 602367806F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4476049 5',
DEFINITION mRNA sequence.

ACCESSION

BG255445

VERSION

BG255445.1

KEYWORDS

EST.

SOURCE

ORGANISM

human.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 522)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: DCPD/DPF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LRAM0302 row: 1 column: 02
High quality sequence stop: 522.

FEATURES

Source

1..522

Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4476049"
/clone_lib="NIH MGC 91"
/issue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC library."

BASE COUNT 126 a 146 c 121 g 129 t
ORIGIN

Query Match

Best Local Similarity

Matches

362; Conservative

0; Mismatches

0; Indels

1; Gaps

1;

Qy 1617 GTGATTTTCAAGAAATCTACAGTCTCGTTGAGACCAACCACTACCTCAGAAAGTGA 1676
Db 1 GTGATTTTCAAGAAATCTACAGTCTCGTTGAGACCAACCACTACCTCAGAAAGTGA 60
Qy 1677 CTGTGGCCCTAGAGGAGGAGAGAGTGAATGATGTTTCAACCTGAGAGAGATCTTGG 1736
Db 61 CTGTGGCCCTAGAGGAGGAGAGAGTGAATGATGTTTCAACCTGAGAGAGATCTTGG 120
Qy 1737 ATGGTCAGAGCTTATGTGACCTCCAGAGCAAGAGAAAGACTTGGCAAGTCTAGGTCC 1796
Db 121 ATGGTCAGAGCTTATGTGACCTCCAGAGCAAGAGAAAGAACTTGGCAAGTCTAGGTCC 180
Qy 1797 TCAATGTCCCAATAGAGCAAGAGCCCAAGCTCTTTCTTTTCTTTTCTTTTGAAGGAG 1856
Db 181 TCAATGTCCCAATAGAGCAAGAGCCCAAGCTCTTTCTTTTCTTTTCTTTTGAAGGAG 239
Qy 1857 TCTTGGCCCTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1916
Db 240 TCTTGGCCCTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 299

Qy 1917 TCTCTGATTCAAACAAATCTCTGCTCAGAGCTCCAGAAATAGCTGGGATTACAGGGCT 1976
Db 300 TCTCTGATTCAAACAAATCTCTGCTCAGAGCTCCAGAAATAGCTGGGATTACAGGGCT 359
Qy 1977 ACACCAACATGCTGCTGCTAATT 1999
Db 360 ACACCAACATGCTGCTGCTAATT 382

RESULT 25

AL844309

LOCUS 606 bp mRNA linear EST 30-JUL-2002
DEFINITION AL844309 pool_FU11b_v_SPC Homo sapiens cDNA, mRNA sequence.

ACCESSION

AL844309

VERSION

AL844309.1

KEYWORDS

EST.

SOURCE

ORGANISM

human.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 606)
Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
Sheridan, E.
Homo sapiens EST sequence
Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name: scd10817.154136A
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool_FU11b_v_SPC cDNA library. Further information can be found
at http://www.sanger.ac.uk/Teams/Team69/.

FEATURES

Source

1..606

Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="pool_FU11b_v_SPC"
/note="Organ: breast; Vector: pZeo-1; Site 1: SphI;
Site 2: SphI; Duclal carcinoma in situ, high-grade, comedo
, from 41 yo female. Library constructed in the laboratory
of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."

BASE COUNT

138 a 186 c 154 g 125 t

ORIGIN

Query Match

Best Local Similarity

Matches

347; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

Qy 925 GCCCTGTGAGACCAATTAATCTGAGCTGGCGATGATCATCTGCTCAAGAGGCC 984
Db 46 GCCCTGTGAGACCAATTAATCTGAGCTGGCGATGATCATCTGCTCAAGAGGCC 105
Qy 985 TGTGTCCTGAGAGGCTGGCCCTGCTGCGAAGATATACCTGAGCTGTG 1044
Db 106 TGTGTCCTGAGAGGCTGGCCCTGCTGCGAAGATATACCTGAGCTGTG 165
Qy 1045 CAGAGACACCACTCAATCGAAGAGCTGAGCAAGCTCTCTGTTTGAAGTGGC 1104
Db 166 CAGAGACACCACTCAATCGAAGAGCTGAGCAAGCTCTCTGTTTGAAGTGGC 225
Qy 1105 AAGAGGAGAGTCTTTCTCAAGTGAAGTCTCCGGAGTCCCTCACTTCAATCAGC 1164
Db 226 AAGAGGAGAGTCTTTCTCAAGTGAAGTCTCCGGAGTCCCTCACTTCAATCAGC 285
Qy 1165 CTGAATGACAGAGCTGTCTTTGATGATGCTTGAAGCCCAAGAGAGGCCAAAGGGA 1224

Db 286 CTGATGACGAAGCTGTCTCTTTGGATGATGCTTACGCGCCAAAGAGAGCCCAAGGA 345

Qy 1225 AACCAAGGCTGCACTGCTTGAAGACCCCAATTCACCTCTGGGCAACCCCA 1273

Db 346 AACCAAGGCTGCACTGCTTGAAGACCCCAATTCACCTCTGGGCAACCCCA 394

RESULT 26

AA310216 281 bp mRNA linear EST 19-APR-1997

DEFINITION EST181048 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA sequence.

AA310216

ACCESSION AA310216 GI:1962543

VERSION EST.

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Well,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marnaros,S.M., Merrick,J.M., Pellegriano,S.M., Moreno-Palenzuela,R.F., McDonald,L.A., Nguyen,D.T., Pelligriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Benharik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.M., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,K., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haelttine,W.A., Fleides,C., Frazer,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

COMMENT Contact: Kerlavage, AR

Bioinformatics for Genomic Research

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@igf.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/cdb/hgt/hgt.html)

Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1..281

/organism="Homo sapiens"

/db_xref="ATCC (inhost):156269"

/db_xref="taxon:9606"

/clone_lib="Jurkat T-cells V"

/cell_type="T-lymphocyte"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 72 a 75 c 81 g 51 t 2 others

ORIGIN

Query Match 5.0%; Score 128; DB 9; Length 281;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 278; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2221 CTTAAGCTTGAACACTGAGTGAAGCCAGGCACTCTAGTCTGGGAGGGGATCAGAA 2280

Db 1 CTTAAGCTTGAACACTGAGTGAAGCCAGGCACTCTAGTCTGGGAGGGGATCAGAA 60

Qy 2281 GGTGCTAAGCCCTCTCTCCACAATGCGAAGACGAGGACCAAGGCTTCAACCAATCGAG 2340

Db 61 GGTGCTAAGCCCTCTCTCTCCACAATGCGAAGACGAGGACCAAGGCTTCAACCAATCGAG 120

Qy 2341 CTTGATTTTCCTGCTGCTTCCTCCATTAACAGAAAGGTGTGCTGATTCGCTAAGGGATC 2400

Db 121 CTTGATTTTCCTGCTGCTTCCTCCATTAACAGAAAGGTGTGCTGATTCGCTAAGGGATC 180

Qy 2401 AGGAGAGGAGAAAGAGAGGATGGGTGGAGGACCCCTCCAGGCTCCCTACTGGTTC 2460

Db 181 AGGAGAGGAGAAAGAGAGGATGGGTGGAGGACCCCTCCAGGCTCCCTACTGGTTC 240

Qy 2461 CCAAGCTACAGGTGGGTGGGAAAGGCTTTATCAGATATCA 2501

Db 241 CCAAGCTACAGGTGGGTGGGAAAGGCTTTATCAGATATCA 281

RESULT 27

B45150 506 bp DNA linear GSS 21-OCT-1997

LOCUS HS-1060-B1-H07-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 782 Col=13 Row=P, DNA sequence.

DEFINITION B45150

ACCESSION B45150

VERSION B45150.1 GI:2549984

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Maharis,G.G., Zackrone,K.D., Smith,T., Tipson,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.

TITLE Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors

JOURNAL Unpublished (1997)

COMMENT Contact: Maharis GG, Zackrone KD, Hood L

University of Washington

Seattle, WA 98195, USA

Tel: (206) 616-8744

Fax: (206) 685-7301

Email: kzackrone@u.washington.edu

Sequence Tagged Connector

Plate: CT 782 Row: P Column: 13

Class: BAC ends

High quality sequence stop: 506.

Location/Qualifiers

1..506

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Plate=CT 782 Col=13 Row=P"

/clone_lib="CIT Human Genomic Sperm Library C"

/sex="M"

/note="Organ: sperm; Vector: pBlotBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 105 a 128 c 161 g 112 t

ORIGIN

Query Match 4.0%; Score 103; DB 17; Length 506;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 AGAGAGAACAGAGGCAAGCAGCCTGAGGAGTTTCCCGAGAGGTGGCGGCGGA 563

Db 210 AGAGAGAACAGAGGCAAGCAGCCTGAGGAGTTTCCCGAGAGGTGGCGGCGGA 269

Qy 564 GCTGTGCTGAGACTCGGGAGGCAATTCATGCTCTCTGAG 606

Db 270 GCTGTGCTGAGACTCGGGAGGCAATTCATGCTCTCTGAG 312

RESULT 28

AI002059/c 110 bp mRNA linear EST 09-JUN-1998

LOCUS OS97A07.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613268 3'

DEFINITION

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208

Email: hbe@tigr.org
Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: 17
Class: BAC ends.

FEATURES

Location/Qualifiers
1..489
/organism="Homo sapiens"
/db_xref="GDB:7542514"
/db_xref="taxon:9606"
/clone="RPCT-11-111L11"
/clone_id="RPCT-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: PBACe3.6; Site 1: EcoRI; Site 2: EcoRI; RRC11 Human Male BAC library"

BASE COUNT

140 a 100 c 102 g 147 t

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2035

TTGGCCAGGCTGTGTCGACCTGACCTGATCCACCACTTGGCTCCCAA 2094

Db 372

TTGGCCAGGCTGTGTCGACCTGACCTGATCCACCACTTGGCTCCCAA 313

Qy 2095

GTGCTGGGATTACA 2108

Db 312

GTGCTGGGATTACA 299

RESULT 31

LOCUS

A0431946 534 bp DNA linear GSS 31-MAR-1999

DEFINITION

HS_5065_A2_F08_T7A_RPCT-11 Human Male BAC Library Homo sapiens genomic clone Plate=641 Col=16 Row=K, DNA sequence.

ACCESSION

A0431946

VERSION

A0431946.1 GI:4542281

KEYWORDS

GSS.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 534)
Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,
Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
Hood L.

AUTHORS

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

TITLE

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

JOURNAL

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCT-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu

COMMENT

Plate: 641 row: K column: 16
Seq primer: 17
Class: BAC ends
High quality sequence stop: 534.
Location/Qualifiers
1..534
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=641 Col=16 Row=K"
/clone_id="RPCT-11 Human Male BAC Library"
/sex="male"
/note="Vector: PBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the PBACe3.6 vector at EcoRI sites"

FEATURES

source

BASE COUNT

144 a 105 c 119 g 155 t 11 others

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2035

TTGGCCAGGCTGTGTCGACCTGACCTGATCCACCACTTGGCTCCCAA 2094

Db 401

TTGGCCAGGCTGTGTCGACCTGACCTGATCCACCACTTGGCTCCCAA 342

Qy 2095

GTGCTGGGATTACA 2108

Db 341

GTGCTGGGATTACA 328

RESULT 32

LOCUS

BG943550 572 bp mRNA linear EST 11-JUN-2001

DEFINITION

ax39b11.x1 Proliferating Human Erythroid Cells (LCB:ax library)
Homo sapiens cDNA clone ax39b11 random, mRNA sequence.

ACCESSION

BG943550

VERSION

BG943550.1 GI:14342922

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 572)
Gubin A.N., Njoroge J.M., Bouffard G.G. and Miller J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)

AUTHORS

Contact: Jeffrey L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
20892, USA
Tel: 301 402 2373
Fax: 301 435 5148

JOURNAL

Email: jlm1@nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 39 row: b column: 11
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1..572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ax39b11"
/clone_id="Proliferating Human Erythroid Cells (LCB:ax library)"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"

COMMENT

TITLE

JOURNAL

COMMENT

TITLE

JOURNAL

COMMENT

TITLE

JOURNAL

COMMENT

TITLE

JOURNAL

COMMENT

TITLE

JOURNAL

COMMENT

TITLE

JOURNAL

COMMENT

```
/dev_stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
/notes="Organ: Blood; Vector: Lambda ZAP II; Site 1: EcoRI;
Site 2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using TRIzol reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's CapFinder cDNA Library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcoRI digested Lambda Zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
throughput (NIH intramural sequencing center
http://www.nigc.nih.gov/)."

BASE COUNT      162 a      122 c      144 g      144 t
ORIGIN

Query Match      2.8%; Score 73; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAATCTCGAGTGTGATCCACCCACCTTGCCCTCCCAAGTGTGGATTACG 2109
Db 375 TCGAATCTCTGAGTGTGATCCACCCACCTTGCCCTCCCAAGTGTGGATTACG 316
Qy 2110 GTGTGAGCCACG 2122
Db 315 GTGTGAGCCACG 303

RESULT 33
AW247089      503 bp      mRNA      linear      EST 07-JAN-2000
LOCUS      2822458.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822458 5'
DEFINITION      mRNA sequence.
ACCESSION      AW247089
VERSION      AW247089.1 GI:6590082
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 503)
AUTHORS      NIH-MGC http://www.ncbi.nlm.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Other ESTs: 2822458.Sprime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (ILNI) DNA Sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/ILNI at:
www.bio.lnl.gov/bdrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PhRAP suite. Poly-T identification: patchmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu
Plate: ILICM9 row: H column: 11
High quality sequence stop: 454.
Location/Qualifiers
1..503
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2822458"
/clone_lib="NIH_MGC_7"
/tissue_type="small_cell carcinoma"
/cell_line="MGC3"

/dev_stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
/notes="Organ: Blood; Vector: Lambda ZAP II; Site 1: EcoRI;
Site 2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using TRIzol reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's CapFinder cDNA Library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcoRI digested Lambda Zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
throughput (NIH intramural sequencing center
http://www.nigc.nih.gov/)."

BASE COUNT      162 a      122 c      144 g      144 t
ORIGIN

Query Match      2.8%; Score 73; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAATCTCGAGTGTGATCCACCCACCTTGCCCTCCCAAGTGTGGATTACG 2109
Db 375 TCGAATCTCTGAGTGTGATCCACCCACCTTGCCCTCCCAAGTGTGGATTACG 316
Qy 2110 GTGTGAGCCACG 2122
Db 315 GTGTGAGCCACG 303

RESULT 34
BQ016908      637 bp      mRNA      linear      EST 17-JUN-2002
LOCUS      BQ016908
DEFINITION      UT-H-DIO-ausz-d-06-0-UT.si NCI CGAP_D10 Homo sapiens cDNA clone
IMAGE:5876309 3', mRNA sequence.
ACCESSION      BQ016908
VERSION      BQ016908.1 GI:19752185
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 637)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNI at: http://image.lnl.gov
The following repetitive elements were found in this cDNA
sequence: 14-143>ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.
Location/Qualifiers
1..637
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5876309"
/clone_lib="NCI_CGAP_D10"
/tissue_type="Lung Focal Fibrosis"
/dev_stage="Adult"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP D10 is a cDNA library containing the following
tissue(s): A pool of Lung Focal Fibrosis. The library was
constructed according to Bonaldi, Lemmon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pRTT3-Pac vector. The oligonucleotide used to prime
```

the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drr)18 tail. The sequence tag for this library is

(drr)18 tail. The sequence tag for this library is

BASE COUNT 148 a 149 c 165 g 174 t 1 others

ATACCGGCTC
TAG_LIB=UI-H-D10
TAG_TISSUE=lung with fibrosis
TAG_SEQ=ATACCGGCTC

Query Match 2.8%; Score 71; DB 14; Length 637;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 2.8%; Score 71; DB 14; Length 671;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAAGCTCTGAGCTGATGATCCACCACTTGCGCTCCCAAGTGTGGATTACAG 2109
DB 62 TCGAAGCTCTGAGCTGATGATCCACCACTTGCGCTCCCAAGTGTGGATTACAG 121
QY 2110 GTGTGAGCCAC 2120
DB 122 GTGTGAGCCAC 132

QY 2050 TCGAAGCTCTGAGCTGATGATCCACCACTTGCGCTCCCAAGTGTGGATTACAG 2109
DB 214 TCGAAGCTCTGAGCTGATGATCCACCACTTGCGCTCCCAAGTGTGGATTACAG 273
QY 2110 GTGTGAGCCAC 2120
DB 274 GTGTGAGCCAC 284

RESULT 35
BM997767 671 bp mRNA linear EST 17-JUN-2002
LOCUS UI-H-D10-aww-i-02-0-UI.s1 NCI_CGAP_D10 Homo sapiens cDNA clone
IMAGE:5875273 3', mRNA sequence.
ACCESSION BM997767
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 671)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cga@nci.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
The following repetitive elements were found in this cDNA
sequence: 8-235, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

RESULT 36
AG010953/ 700 bp DNA linear GSS 14-APR-1999
LOCUS AG010953
DEFINITION Homo sapiens genomic DNA, 21q region, clone: S594BG38, genomic
survey sequence.
ACCESSION AG010953 AG004614
VERSION AG010953.1 GI:3347781
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone: S594BG38.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 700)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
REFERENCE 2 (bases 1 to 700)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
JOURNAL Direct Submission
COMMENT Submitted (28-JUL-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail: hattori@hgc.jst.go.jp, Tokyo, Japan).
Tel: 0427-78-9732, Fax: 0427-78-9561
On Feb 5, 1999 this sequence version replaced gi:2822077.
AG004614: Submitted (29-Jan-1998).

JOURNAL COMMENT
CONTACT: Robert Strauberg, Ph.D.
Email: cga@nci.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
The following repetitive elements were found in this cDNA
sequence: 8-235, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

JOURNAL COMMENT
CONTACT: Robert Strauberg, Ph.D.
Email: cga@nci.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
The following repetitive elements were found in this cDNA
sequence: 8-235, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
SOURCE Location/Qualifiers
1..671
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5875273"
/clone_lib="NCI_CGAP_D10"
/issue_type="Lung Focal Fibrosis"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI CGAP D10 is a cDNA library containing the following
tissue(s): A pool of lung focal fibrosis. The library was
constructed according to Bonaldi, Lemmon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecor I
adaptor, digested with Not I, and cloned directionally
into p773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the

BASE COUNT 149 a 161 c 178 g 143 t 69 others

Query Match 2.8%; Score 71; DB 17; Length 700;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAAGCTCTGAGCTGATGATCCACCACTTGCGCTCCCAAGTGTGGATTACAG 2109
DB 335 TCGAAGCTCTGAGCTGATGATCCACCACTTGCGCTCCCAAGTGTGGATTACAG 276
QY 2110 GTGTGAGCCAC 2120
DB 275 GTGTGAGCCAC 265

RESULT 37 737 bp mRNA linear EST 20-OCT-2000
LOCUS BE904397
DEFINITION 601496313p1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898443 5',

```

ACCESSION      mRNA sequence.
VERSION        BE904397.1 GI:10396608
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE         NIH-MGC http://mgi.nci.nih.gov/
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgaabs-r@mail.nih.gov
                Tissue Procurement: ATCC
                CDNA Library Preparation: Life Technologies, Inc.
                CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLM9694 row: i column: 04
                High quality sequence stop: 673.
                Location/Qualifiers
                source
                1..737
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:3898443"
                /clone_1db="NIH_MGC_70"
                /tissue_type="epithelioid carcinoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: pancreas; Vector: pCMV-Sport6; Site 1: NotI;
                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.1 Kb. Library constructed by Life
                Technologies."
BASE COUNT      162 a 187 c 196 g 192 t
ORIGIN
Query Match    2.8%; Score 71; DB 12; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2050 TCGAAGCTCTGAGCTGATCCACCCACCTTGGCTCCCAAGTCTGGATTACAG 2109
         |||||
DB 216 TCGAAGCTCTGAGCTGATCCACCCACCTTGGCTCCCAAGTCTGGATTACAG 275
QY 2110 GTGTGAGCCAC 2120
         |||||
DB 276 GTGTGAGCCAC 286

RESULT 38
BF664472      832 bp mRNA linear EST 21-DEC-2000
LOCUS         60214624F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4309876 5',
DEFINITION    mRNA sequence.
ACCESSION     BF664472
VERSION       BF664472.1 GI:11938277
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE         NIH-MGC http://mgi.nci.nih.gov/
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgaabs-r@mail.nih.gov
                Tissue Procurement: ATCC
                CDNA Library Preparation: Life Technologies, Inc.
                CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLM9694 row: i column: 13
                High quality sequence stop: 733.
                Location/Qualifiers
                source
                1..896
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4853076"
                /clone_1db="NIH_MGC_48"
                /tissue_type="primary B-cells from tonsils (cell line)"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: B-cells; Vector: pOT87; Site 1: XhoI;
                Site 2: EcoRI; CDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCAGAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."
BASE COUNT      168 a 221 c 228 g 215 t
ORIGIN
Query Match    2.8%; Score 71; DB 12; Length 832;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2050 TCGAAGCTCTGAGCTGATCCACCCACCTTGGCTCCCAAGTCTGGATTACAG 2109
         |||||
DB 253 TCGAAGCTCTGAGCTGATCCACCCACCTTGGCTCCCAAGTCTGGATTACAG 312
QY 2110 GTGTGAGCCAC 2120
         |||||
DB 313 GTGTGAGCCAC 323

RESULT 39
BG758454      896 bp mRNA linear EST 15-MAY-2001
LOCUS         602712653F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4853076 5',
DEFINITION    mRNA sequence.
ACCESSION     BG758454
VERSION       BG758454.1 GI:14069107
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE         NIH-MGC http://mgi.nci.nih.gov/
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgaabs-r@mail.nih.gov
                Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
                CDNA Library Preparation: Ling Hong/Rubin Laboratory
                CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLM9694 row: i column: 13
                High quality sequence stop: 733.
                Location/Qualifiers
                source
                1..896
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4853076"
                /clone_1db="NIH_MGC_48"
                /tissue_type="primary B-cells from tonsils (cell line)"
                /lab_host="DH10B (phage-resistant)"

```


/note="Organ: B-cell19; Vector: pOT87; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MCC Library."

BASE COUNT 206 a 219 c 240 g 231 t
ORIGIN

Query Match 2.8%; Score 71; DB 12; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAATCTGACCTGAGTGTACACCCCTTGCTCCCAAGTCTGGGATTACAGT 2109
Db 257 TCGAATCTGACCTGAGTGTACACCCCTTGCTCCCAAGTCTGGGATTACAGT 316

Qy 2110 GTGTAGCCAC 2120
Db 317 GTGTAGCCAC 327

RESULT 40
LOCUS A0261419/c 581 bp DNA linear GSS 24-OCT-1998
DEFINITION CITBI-E1-2509P17.TF CITBI-E1 Homo sapiens genomic clone 2509P17,
DNA sequence.
ACCESSION A0261419
VERSION A0261419.1 GI:3787943
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Adams,M.D., Rounsailey,S.D., Zhao,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.

TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building

JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CITBI-E1-2509P17.TF

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES location/Qualifiers

1..581
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2509P17"
/clone_1ib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 180 a 131 c 151 g 119 t
ORIGIN

Query Match 2.7%; Score 69; DB 17; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2052 GAATCTCTACTAGGTGATCCACCCCTTGAGCTTCCCAAGTCTGGGATTACAGT 2111
Db 511 GAATCTCTACTAGGTGATCCACCCCTTGAGCTTCCCAAGTCTGGGATTACAGT 452

Qy 2112 GTGAGCCAC 2120
Db 451 GTGAGCCAC 443

RESULT 41
LOCUS A0542542 596 bp DNA linear GSS 19-MAY-1999
DEFINITION RPCI-11-347J18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-347J18
, DNA sequence.

ACCESSION A0542542 GI:4872998
VERSION A0542542.1
KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 596)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.C.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building

JOURNAL Unpublished (1997)
COMMENT Other_GSSs: RPCI-11-347J18.TV

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@tigr.org, med.buffalo.edu). Clones may be purchased from
BACRAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES location/Qualifiers

1..596
/organism="Homo sapiens"
/db_xref="GB:7633097"
/db_xref="taxon:9606"
/clone="RPCI-11-347J18"
/clone_1ib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"

BASE COUNT 145 a 143 c 109 g 198 t 1 others
ORIGIN

Query Match 2.7%; Score 69; DB 17; Length 596;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2052 GAATCTCTACTAGGTGATCCACCCCTTGAGCTTCCCAAGTCTGGGATTACAGT 2111
Db 503 GAATCTCTACTAGGTGATCCACCCCTTGAGCTTCCCAAGTCTGGGATTACAGT 562

Qy 2112 GTGAGCCAC 2120
Db 563 GTGAGCCAC 571

RESULT 42
A0346722/c

LOCUS AQ348722 617 bp DNA linear GSS 07-MAY-1999
 DEFINITION RPEC11-11617.TU RPEC1-11 Homo sapiens genomic clone RPEC1-11-11617,
 DNA sequence.
 ACCESSION AQ348722
 VERSION AQ348722.1 GI:4173618
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 617)
 Zhao, S., Adams, M. D., Niernan, W., Malek, J., de Jong, P. and Venter
 J.C.
 TITLE Use of BAC End Sequences from Library RPEC1-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSE: RPEC11-11617.TU
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPEC1-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/>) or from
 Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 1..617
 /organism="Homo sapiens"
 /db_xref="GDB:7544358"
 /db_xref="taxon:9606"
 /clone="RPEC1-11-11617"
 /clone_1ib="RPEC1-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site 1: EcoRI, Site 2: EcoRI;
 RPEC11 Human Male BAC library"
 BASE COUNT 143 a 140 c 142 g 192 t
 ORIGIN

Query Match 2.7%; Score 69; DB 17; Length 617;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2052 GAATCTGAGCTGATGATCCACCCACCTTGCCCTCCCAAGTGGGATTACAGGT 2111
 |||||||
 Db 291 GAATCTGAGCTGATGATCCACCCACCTTGCCCTCCCAAGTGGGATTACAGGT 232
 |||||||

Qy 2112 GTGAGCCAC 2120
 |||||||
 Db 231 GTGAGCCAC 223
 |||||||

RESULT 43
 LOCUS AI902426 262 bp mRNA linear EST 30-MAR-2000
 DEFINITION CM-BT006-080299-139 BT006 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AI902426
 VERSION AI902426.1 GI:6492813
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 262)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matakuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brenham, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/seq/gethtml.pl?cl=CM2-CM-BT006-139.html>)
 (ct3=080299ct4=1)
 Seq primer: puc 18 forward.
 Location/Qualifiers
 1..262
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1ib="BT006"
 /sex="Female"
 /dev_stage="Adult"
 /note="Organ: breast; Vector: puc18; Site 1: SmaI, Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 '716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT 83 a 58 c 68 g 44 t 9 others
 ORIGIN

Query Match 2.6%; Score 68; DB 9; Length 262;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2053 AACTCTGAGCTGATGATCCACCCACCTTGCCCTCCCAAGTGGGATTACAGGTG 2112
 |||||||
 Db 193 AACTCTGAGCTGATGATCCACCCACCTTGCCCTCCCAAGTGGGATTACAGGTG 134
 |||||||

Qy 2113 TGAGCCAC 2120
 |||||||
 Db 133 TGAGCCAC 126
 |||||||

RESULT 44
 LOCUS BF753734 420 bp mRNA linear EST 10-JAN-2001
 DEFINITION IL5-CT0521-031000-163-f02 CT0521 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF753734
 VERSION BF753734.1 GI:12080410
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 420)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matakuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brenham, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663

COMMENT

Contact: Simeon A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimeon@ludwig.org.br

This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=115&t=115-CT0521-
031000-163-f02&t3=2000-10-03&t4=1)

Seq primer: puc 18 forward
High quality sequence stop: 418.

FEATURES

source

Location/Qualifiers
1..420

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="CT0521"
/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
.716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 127 a 86 c 113 g 94 t
ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2053 AACTCTGACCTGAGTATCCACCCACCTGCTCCCAAGTCTGGATTACAGTG 2112
LOCUS
Db 243 AACCTCGACCTGAGTATCCACCCACCTGCTCCCAAGTCTGGATTACAGTG 184
QY 2113 TGAGCCAC 2120
Db 183 TGAGCCAC 176

RESULT 45

AQ583583 436 bp DNA linear GSS 07-JUN-1999
LOCUS
DEFINITION
RPCI-11-454D13.TV RPCI-11 Homo sapiens genomic clone RPCI-11-454D13
/ DNA sequence.

ACCESSION
KEYWORDS
Q583583.1 GI:5010693

SOURCE

ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 436)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.C.

REFERENCE
AUTHORS
J.C.

TITLE

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)

JOURNAL
COMMENT
Other GSSs: RPCI-11-454D13.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208

Email: hbeet@igf.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet. Co. (info@regen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1..436

/organism="Homo sapiens"
/db_xref="GDB:7674036"
/db_xref="taxon:9606"
/clone="RPCI-11-454D13"
/clone_id="RPCI-11"
/sex="Male"

/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC library"

BASE COUNT 75 a 146 c 91 g 121 t 1 others
ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2053 AACTCTGACCTGAGTATCCACCCACCTGCTCCCAAGTCTGGATTACAGTG 2112
LOCUS
Db 83 AACCTCGACCTGAGTATCCACCCACCTGCTCCCAAGTCTGGATTACAGTG 142
QY 2113 TGAGCCAC 2120
Db 143 TGAGCCAC 150

RESULT 46

AQ462891 531 bp DNA linear GSS 23-APR-1999
LOCUS
DEFINITION
HS 5212 At B12 T7A RPCI-11 Human Male BAC library Homo sapiens
genomic clone Plate=788 Col=23 Row=C, DNA sequence.

ACCESSION
VERSION
Q462891.1 GI:4635661

SOURCE

ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 531)

REFERENCE
AUTHORS
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

CONTACT: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Research Genetics (info@regen.com). BAC end Web Server:
http://www.htsc.washington.edu

Plate: 788 Row: C Column: 23
Seq primer: T7
Class: BAC ends
High quality sequence stop: 531.

Location/Qualifiers
1..531

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=788 Col=23 Row=C"

FEATURES
source

/clone.lib="RP43-11 Human Male BAC library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"
 BASE COUNT 148 a 123 c 101 g 146 t 13 others
 ORIGIN

Query Match 2.6%; Score 68; DB 17; Length 531;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2053 AACTCTGACCTGAGTATCCACCCAGCTGGCTCCCAAGTGGATTACAGGTG 2112
 |||||
 DB 432 AACTCTGACCTGAGTATCCACCCAGCTGGCTCCCAAGTGGATTACAGGTG 491
 |||||
 OY 2113 TGAGCCAC 2120
 |||||
 DB 492 TGAGCCAC 499

RESULT 47
 AOS56467 546 bp DNA linear GSS 29-MAY-1999
 LOCUS HS_5236_B1_C01_T7A RP43-11 Human Male BAC library Homo sapiens
 DEFINITION genomic clone Plate=812 Col=1 Row=F, DNA sequence.

ACCESSION AOS56467
 VERSION AOS56467.1 GI:4916199
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 546)

AUTHORS Mahaitas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahaitas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RP43-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Research Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 Plate: 812 row: F column: 1
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 546.
 Location/Qualifiers

FEATURES
 source
 1. 546
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="plate=812 Col=1 Row=F"
 /clone.lib="RP43-11 Human Male BAC library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"
 BASE COUNT 135 a 120 c 173 g 108 t 10 others

ORIGIN

Query Match 2.6%; Score 68; DB 17; Length 546;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 372 ATTTCCTGATATGCTTCTGAGTGTCTGAGGAACAATGAGTCCCGAG 431
 |||||
 DB 383 ATTTCCTGATATGCTTCTGAGTGTCTGAGGAACAATGAGTCCCGAG 442
 |||||
 OY 432 CAGAGAA 439
 |||||
 DB 443 CAGAGAA 450

RESULT 48
 AG144939/c 701 bp DNA linear GSS 08-JAN-2002
 LOCUS AG144939/c
 DEFINITION Pan troglodytes DNA, clone: RP43-006B10.T7, genomic survey
 sequence.
 ACCESSION AG144939
 VERSION AG144939.1 GI:16674617
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphocytes DNA, clone lib:RP43-43 Chimpanzee
 Male BAC library clone:RP43-006B10.T7.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Toooki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of library RP43-43
 2 (bases 1 to 701)

AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Toooki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Direct Submision
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpanzee@resgen.com, riken-go.jp, URL: http://hgp.gsc.riken-go.jp/
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT Clones are derived from the chimpanzee BAC library RP43-43 This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: T7
 LIBRARY
 Vector : pBAC3.6
 R Site 1 : EcoRI
 R Site 2 : EcoRI

FEATURES

source
 1. 701
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="RP43-006B10.T7"
 /sex="male"
 /cell type="lymphocytes"
 /clone.lib="RP43-43 Chimpanzee Male BAC library"
 BASE COUNT 212 a 145 c 159 g 185 t
 ORIGIN

Query Match 2.6%; Score 68; DB 17; Length 701;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2053 AACTCTGACCTGAGTATCCACCCAGCTGGCTCCCAAGTGGATTACAGGTG 2112
 |||||
 DB 194 AACTCTGACCTGAGTATCCACCCAGCTGGCTCCCAAGTGGATTACAGGTG 135
 |||||
 OY 2113 TGAGCCAC 2120
 |||||
 DB 134 TGAGCCAC 127

RESULT 49
 BG71899/c 742 bp mRNA linear EST 08-MAY-2001
 LOCUS 60269911f1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831083 5',
 DEFINITION mRNA sequence.
 ACCESSION BG718999
 VERSION BG718999
 KEYWORDS EST.
 SOURCE BG718999.1 GI:13998186
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 742)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgapdb-remail.nih.gov
 Issue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM10753 row: e column: 04
 High quality sequence stop: 740.
 Location/Qualifiers
 1..742
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4831083"
 /clone_lib="NIH_MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescript (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
 size selected for average insert size 2.2 kb and
 normalized to ROT 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
 BASE COUNT 232 a 167 c 144 g 199 t
 ORIGIN

Query Match 2.6%; Score 66; DB 12; Length 742;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 CTCCTGACCTCAGGTGATCCACCCACCTTGCCCAAGTGTGGATTACAGGTGTG 2114
 |||||
 DB 671 CTCCTGACCTCAGGTGATCCACCCACCTTGCCCAAGTGTGGATTACAGGTGTG 612
 |||||
 QY 2115 AGCCAC 2120
 |||||
 DB 611 AGCCAC 606

RESULT 50
 AG675390/c 472 bp DNA linear GSS 24-JUN-1999
 LOCUS AG675390
 DEFINITION HS 2151 Al D03 TTC CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate-2151 Col=5 Row=G, DNA sequence.
 ACCESSION AG675390
 VERSION AG675390.1 GI:5208136
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 472)
 Mammals; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallaceu.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 2151 row: G column: 5
 Seq primer: 17
 Class: BAC ends
 High quality sequence stop: 472.
 Location/Qualifiers
 1..472
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=2151 Col=5 Row=G"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBlotBAC11; BAC Clones in
 E-Coli DH10B"
 BASE COUNT 143 a 73 c 95 g 158 t 3 others
 ORIGIN

Query Match 2.5%; Score 65; DB 17; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2056 TCCGACCTCAGGTGATCCACCCACCTTGCCCAAGTGTGGATTACAGGTGTGA 2115
 |||||
 DB 356 TCCGACCTCAGGTGATCCACCCACCTTGCCCAAGTGTGGATTACAGGTGTGA 297
 |||||
 QY 2116 GCCAC 2120
 |||||
 DB 296 GCCAC 292

RESULT 51
 AUI5455 579 bp mRNA linear EST 05-AUG-2002
 LOCUS AUI5455
 DEFINITION AUI5455 HEMBAI Homo sapiens cDNA clone HEMBAI004880 3', mRNA
 sequence.
 ACCESSION AUI5455
 VERSION AUI5455.1 GI:11006976
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 579)
 Oca, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano
 S. and Iwagai, T.).
 HRI human cDNA project (Oca, T., Nishikawa, T., Suzuki, Y., Ishii, S.,
 Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura
 Y., Nagai, T., Sugano, S., Iwagai, T.)
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Iwagai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986

Email: genomics@ri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

source

Location/Qualifiers
 1. 579
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEMBA1004880"
 /clone_1ib="HEMBA1"
 /tissue_type="whole embryo, mainly head"
 /note="stage=embryo, 10 weeks"
 /note="Vector: pME18SFL3"

BASE COUNT 146 a 133 c 111 g 181 t 8 others
 ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

Qy

2056 TCTGACCTCAGGTGATCCACCCACCTTGCGCTCCAAAGTGTGAGTTACAGGTGTGA 2115
 329 TCTGACCTCAGGTGATCCACCCACCTTGCGCTCCAAAGTGTGAGTTACAGGTGTGA 388

Db

Qy

2116 GCCAC 2120
 389 GCCAC 393

RESULT 52

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

N22395 448 bp mRNA linear EST 20-DEC-1995
 yw3f08.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
 IMAGE:254439 3' similar to contains Alu repetitive element, mRNA
 sequence.
 N22395
 EST
 N22395.1 GI:1128529
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 448)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
 Chisoso, S., Dietrich, N., Dubuque, T., Pavello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierrey-Meg, J., Trevisan, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence STOPS: 346
 Source: IMAGE Consortium, LNLN
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 844 Std Error: 0.00
 Seq primer: ml3 -40 forward
 High quality sequence STOPS: 346.
 Location/Qualifiers

FEATURES

source

1. 448
 /organism="Homo sapiens"
 /db_xref="GDB:3891892"
 /db_xref="taxon:9606"
 /clone="IMAGE:254439"
 /clone_1ib="Morton Fetal Cochlea"

/tissue_type="cochlea"

/dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: ear; Vector: pBluescript SK-; Site: 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
 37% of inserts < 0.5 kb. 56% 0.5-1.0 kb. 7% > 1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAAATTCGACGAG 3' -3' adaptor
 sequence: 5' CTGAGTCTTTTCTTTTCTTTT 3'."
 BASE COUNT 124 a 105 c 94 g 122 t 3 others
 ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

Qy

2058 CTGACCTCAGGTGATCCACCCACCTTGCGCTCCAAAGTGTGAGTTACAGGTGTGA 2117
 214 CTGACCTCAGGTGATCCACCCACCTTGCGCTCCAAAGTGTGAGTTACAGGTGTGA 273

Db

Qy

2118 CAC 2120
 274 CAC 276

RESULT 53

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AO531017 457 bp DNA linear GSS 18-MAY-1999
 RPCI-11-373D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-373D14
 , DNA sequence.
 AO531017
 GSS.
 AO531017.1 GI:4843060
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 457)
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
 Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other GSSs: RPCI-11-373D14.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@jeon.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genes (http://info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: 17
 Class: BAC ends.
 Location/Qualifiers

FEATURES

source

1. 457
 /organism="Homo sapiens"
 /db_xref="GDB:7642933"
 /db_xref="taxon:9606"
 /clone="RPCI-11-373D14"
 /clone_1ib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site: 1: EcoRI, site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 BASE COUNT 127 a 79 c 115 g 136 t

Query Match 2.5%; Score 63; DB 17; Length 457;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2058 CTGACCTCAGTGATCCACCCACCTGGCTCCCAAGTCTGGATTACAGTGTGAGC 2117

Db 286 CTGACCTCAGTGATCCACCCACCTGGCTCCCAAGTCTGGATTACAGTGTGAGC 227

Qy 2118 CAC 2120

Db 226 CAC 224

RESULT 54

LOCUS

DEFINITION RPT-11-475A11.TV RPT-11 Homo sapiens genomic clone RPT-11-475A11

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Shaying Zhao, William Niernan, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeet@igrr.org

Clones are derived from the human BAC library RPT-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet. Co. (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search.html.

Seq primer: 17

Class: BAC ends.

Location/Qualifiers

1..621

/organism="Homo sapiens"

/db_xref="GDB:7682026"

/db_xref="taxon:9606"

RESULT 55

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Shaying Zhao, William Niernan, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeet@igrr.org

Clones are derived from the human BAC library RPT-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet. Co. (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search.html.

Seq primer: 17

Class: BAC ends.

Location/Qualifiers

1..433

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="CT0364"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site 1: Sma1; Site 2:

Sma1; A mini-library was made by cloning products derived

from ORSTES PCR (U.S. Letters Patent application No. 196

Qy 2059 TGACCTCAGTGATCCACCCACCTGGCTCCCAAGTCTGGATTACAGTGTGAGC 2118

Db 171 TGACCTCAGTGATCCACCCACCTGGCTCCCAAGTCTGGATTACAGTGTGAGC 112

Qy 2119 AC 2120

Db 111 AC 110

RESULT 56

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Shaying Zhao, William Niernan, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeet@igrr.org

Clones are derived from the human BAC library RPT-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet. Co. (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search.html.

Seq primer: 17

Class: BAC ends.

Location/Qualifiers

1..433

/organism="Homo sapiens"

/db_xref="taxon:9606"

Qy 2112 GTG 2114

Db 282 GTG 284

Qy 2112 GTG 2114

Db 282 GTG 284

RESULT 57

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Shaying Zhao, William Niernan, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeet@igrr.org

Clones are derived from the human BAC library RPT-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet. Co. (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search.html.

Seq primer: 17

Class: BAC ends.

Location/Qualifiers

1..433

/organism="Homo sapiens"

/db_xref="taxon:9606"

VERSION AQ343967.1 GI:4168863
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 543)
 REFERENCE Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
 TITLE Use of BAC End Sequences from library RPCI-11 for Sequence-Ready Map Building (1997)
 JOURNAL Unpublished
 COMMENT Other GSSs: RPCI11-112016.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0208
 Fax: 301 838 0208
 Email: hbe@igr.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jlong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.igr.org/cdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 1..543
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="GDB:7542855"
 /db_xref="taxon:9606"
 /clone_lib="RPCI-11-112016"
 /clone_1ib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; PCII1 Human Male BAC Library"

BASE COUNT 127 a 138 c 131 g 147 t

ORIGIN

Query Match 2.4%; Score 62; DB 17; Length 543;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2059 TGACCTGAGTGATCCACCCACCTTGCCCTCCCAAAGTGTGGATTACAGTGTGAGCC 2118
 |||
 DB 359 TGACCTGAGTGATCCACCCACCTTGCCCTCCCAAAGTGTGGATTACAGTGTGAGCC 418

OY 2119 AC 2120
 ||
 DB 419 AC 420

RESULT 57
 AQ435006 593 bp DNA linear GSS 31-MAR-1999
 LOCUS HS_3114_82_A08.T7A RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=690 Col=16 Row=B, DNA sequence.
 ACCESSION AQ435006
 VERSION AQ435006.1 GI:4546345
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 593)
 REFERENCE Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Koller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jlong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end web server: http://www.htsc.washington.edu
 Plate: 690 row: B column: 16
 Seq primer: 17
 Class: BAC ends
 High quality sequence stop: 593.

FEATURES
 source
 1..593
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="Male"
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

BASE COUNT 150 a 158 c 117 g 142 t 26 others

ORIGIN

Query Match 2.4%; Score 62; DB 17; Length 593;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2059 TGACCTGAGTGATCCACCCACCTTGCCCTCCCAAAGTGTGGATTACAGTGTGAGCC 2118
 |||
 DB 337 TGACCTGAGTGATCCACCCACCTTGCCCTCCCAAAGTGTGGATTACAGTGTGAGCC 278

OY 2119 AC 2120
 ||
 DB 277 AC 276

RESULT 58
 AM470105 174 bp mRNA linear EST 24-FEB-2000
 LOCUS x129g12.x1 NCI_CGAP ut4 Homo sapiens cDNA clone IMAGE:2761606 3'
 DEFINITION similar to contains Alu repetitive element; contains element MER35 repetitive element; mRNA sequence.
 ACCESSION AM470105
 VERSION AM470105.1 GI:7040211
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 174)
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 Tumor Gene Index
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: c9abds-remail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

Found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: 40bp from Gibco
High quality sequence stop: 137.

FEATURES

1. 174

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NCI CGAP-Ut4"

/tissue_type="serous papillary carcinoma, high grade, 2

pooled tumors

/lab_host="DH10B"

/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: Sall;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

BASE COUNT

28 a 45 c 40 g 61 t

ORIGIN

Query Match

Best local similarity: 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

2050 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 2109

Qy

51 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 110

Db

2110 G 2110

Qy

111 G 111

RESULT 59

AA748840

LOCUS

AA748840 214 bp mRNA linear EST 16-JAN-1998

DEFINITION

ny76706.s1 NCI CGAP GCBI Homo sapiens CDNA clone IMAGE:1284227 3,
similar to contains Alu repetitive element; contains element PTRS

ACCESSION

AA748840

VERSION

AA748840.1 GI:2788798

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 214)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strauberg, Ph.D.
Email: cgaabs-remail.nih.gov

Tissue Procurement:

Louis M. Straud, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.

CDNA Library Preparation:

M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by:

Greg Lennon, Ph.D.

DNA Sequencing by:

Washington University Genome Sequencing Center
Cloned through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: 40m13 fwd. ET from Amersham
High quality sequence stop: 196.

Location/Qualifiers

1. 214

FEATURES

/organism="Homo sapiens"

SOURCE

/db_xref="taxon:9606"

clone_lib="NCI CGAP GCBI"

/tissue_type="germinal center B cell"

lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Straud (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer

15'-GTTTACCAATCTGAGTGGAGGAGGCGGCTCATTTTCTTTT-3'
(pharmacia), digested with Not I and Eco RI adaptors
(pharmacia), digested with Not I and Eco RI adaptors
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 42 a 62 c 52 g 58 t

ORIGIN

Query Match 2.4%; Score 61; DB 9; Length 214;

Best local similarity: 100.0%; Pred. No. 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 148 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 207

Qy 2110 G 2110

Db 208 G 208

RESULT 60

BI024997/c 234 bp mRNA linear EST 14-JUN-2001

LOCUS

CM4-MT0286-010201-837-d01 MT0286 Homo sapiens CDNA, mRNA sequence.

DEFINITION

BI024997

ACCESSION

BI024997.1 GI:14431627

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 234)

Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,

Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,

Goldman G.H., Carvalho A.F., Matsumura A., Bala G.S., Simpson D.H.,

Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare

M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and

Simpson A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?PL=CM4&L2=CM4-MT0286-010201-837-d01&L3=2001-02-01&L4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 29

Location/Qualifiers

1. 234

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="MT0286"

/dev_stage="Adult"

/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:

SmaI; A mini-library was made by cloning products derived


```

      /db_xref="taxon:9606"
      /clone_image="1252051"
      /clone_1db="NCBI CGAP GCBI"
      /tissue_type="germinal center B cell"
      /lab_host="DH10B"
      /note="vector: pT73p-Bac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CGBR). cDNA synthesis was
primed with a Not I - oligo(dT) primer
5'-TGTACCACTCGATGAGGAGCGCGCCCTCTTTTTTTTTTTTTT-3'
1). Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

Qy 2050 TCGAAGCTCTGACCTAGAGTGATCCACCCACCTTGCGCTCCCAAGAGCGTGGATTACAG 2109
 Db 148 TCGAAGCTCTGACCTAGAGTGATCCACCCACCTTGCGCTCCCAAGAGCTGGATTACAG 207
 Qy 2110 G 2110
 Db 208 G 208

RESULT 66
BF431825 LOCUS
DEFINITION
nab50h08.x1 Soares_NSF_F8_9M_OT_PA_P.S1 Homo sapiens cDNA clone IMAGE:3289606 3 similar to contains Alu repetitive element /contains element MER2 repetitive element ; , mRNA sequence.
ACCESSION
BF431825
VERSION
BF431825.1 GI:11443939
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 405)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40up from Gldco
High quality sequence stop: 385.
Location/Qualifiers
1..405
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone=IMAGE:3289606"
/clone_lib="Soares_NSF_F8_9M_OT_PA_P.S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and 66 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following:

BASE COUNT	83 a	113 c	84 g	125 t
ORIGIN				
Query Match	2.4%	Score 61;	DB 12;	Length 405;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches	61;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY 2050	TCGAACCTCTGACCTCGAGTGATCCACCCACCTTGCCCTCCCAAGCTCGGAGTTACAG	2109		
Db 207	TCGAACCTCTGACCTCGAGTGATCCACCCACCTTGCCCTCCCAAGCTCGGAGTTACAG	266		
QY 2110	G 2110			
Db 267	G 267			
RESULT 67				
LOCUS	BE169632	412 bp	mRNA	linear
DEFINITION	PM1-HT0527-280200-005-b12 HT0527 Homo sapiens cDNA, mRNA sequence.			EST 21-JUN-2000
ACCESSION	BE169632			
VERSION	BE169632.1	GI:8623253		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (Bases 1 to 412)			
AUTHORS	Dias Neto, E., Garcia Correa R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	20202663			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PAPERP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/genhtml2.pl?l=atc2-PM1-HT0527-280200-005-b12&t3=2000-02-28&t4=1) Seq primer: puc 18 forward High quality sequence start: 216 High quality sequence stop: 216 Location/Qualifiers 1..412 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HT0527" /dev_stage="Adult" /note="Organ: head neck; Vector: puc18; site 1: Sma1; site 2: Sma1; A mini-library was made by cloning applications derived from ORSERTS PCR (U.S. letters Patent applications No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under			

BASE COUNT	83	a	113	c	84	g	125	t
ORIGIN								
Query Match	2.4%; Score 61; DB 12; Length 405;							
Best Local Similarity	100.0%; Pred. No. 0;							
Matches 61; Conservative	0; Mismatches 0; Indels 0; Gaps 0;							
QY 2050	TCGAAGCCCGACGACCGAGGATCCACCCACCTTGCGCTCCCGAAGCGCGGATTACAG 2109							
DB 207	TCGAAGCTCCGACCTCGACGTGATCCACCCACCTTGGCGCTCCCGAAGGTCGTGGATTACAG 266							
QY 2110	G 2110							
Db 267	G 267							
RESULT 67								
BE169632								
LOCUS	412 bp mRNA linear EST 21-JUN-2000							
DEFINITION	BE169632 PM1-HT0527-280200-005-b12 HT0527 Homo sapiens cDNA, mRNA sequence.							
ACCESSION	BE169632							
VERSION	BE169632.1 GI:8623253							
KEYWORDS	EST.							
SOURCE	human.							

RESULT 67	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
BE169632	LOCUS	PM1-870527-280200-005-b12 HT0527 Homo sapiens cDNA, mRNA sequence.	412 bp	mRNA	linear	EST 21-JUN-2000						
BE169632	DEFINITION	PM1-870527-280200-005-b12 HT0527 Homo sapiens cDNA, mRNA sequence.										
BE169632	VERSION	BE169632.1	GI:8632353									
BE169632	KEYWORDS	EST.										
BE169632	SOURCE	human.										
BE169632	ORGANISM	Homo sapiens										
BE169632	REFERENCE	Emkarayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.										
BE169632	AUTHORS	1 (Bases 1 to 412) Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordini, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J. V.										
BE169632	TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags										
BE169632	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)										
BE169632	MEDLINE	20202663										
BE169632	COMMENT	Contact: Simpson A.J.V. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l=kr2=PM1-HT0527-280200-005-b12&ct3=2000-02-28&ct4=1) Seq primer: puc 18 forward High quality sequence start: 27 High quality sequence stop: 216. Location/Qualities 1..412 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_1lb="HT0527" /dev_stage="Adult" /note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSSTS PCR (U.S. letters patent applications No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under										

TITLE
 Quackenbush, J.
 Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray
 Unpublished (2000)
 COMMENT
 Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 286
 Seq primer: Forward.

FEATURES
 source
 1. 501
 Location/Qualifiers

BASE COUNT
 ORIGIN
 119 a 128 c 150 g 104 t

Query Match
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGGGATTACAG 2109
 Db 188 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGGGATTACAG 129

QY 2110 G 2110
 Db 128 G 128

RESULT 73
 AW753552 568 bp mRNA linear EST 28-APR-2000
 LOCUS
 DEFINITION PM3-CT0264-151099-001-g05 CT0264 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW753552
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 568)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM3&ct2=PM3-CT0264-
 151099-001-g05&ct3=1999-10-15&ct4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 9
 High quality sequence stop: 537.
 Location/Qualifiers

FEATURES

source

1. 568
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="CT0264"
 /dev_stage="Adult"
 /note="Organ: colon; Vector: puc18; Site 1: Sma1; Site 2:
 Sma1; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT
 ORIGIN
 140 a 118 c 112 g 198 t

Query Match
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGGGATTACAG 2109
 Db 164 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGGGATTACAG 223

QY 2110 G 2110
 Db 224 G 224

RESULT 74
 AW806847 613 bp mRNA linear EST 17-MAY-2000
 LOCUS
 DEFINITION MR0-ST0020-201099-003-b12 ST0020 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW806847
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 613)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR0-ST0020-201
 099-003-b12&ct3=1999-10-20&ct4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 47
 High quality sequence stop: 594.
 Location/Qualifiers

FEATURES
 source

1. 613
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="ST0020"
 /dev_stage="Adult"
 /note="Organ: stomach; Vector: puc18; Site 1: Sma1;
 Site 2: Sma1; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 142 a 149 c 193 g 129 t

Query Match 2.4%; Score 61; DB 10; Length 613;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2052 GAACCTCTGACCTGAGTATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAGT 2111

Db 433 GAACCTCTGACCTGAGTATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAGT 374

OY 2112 G 2112

Db 373 G 373

RESULT 75

AV733872/c 618 bp mRNA linear EST 17-OCT-2000

LOCUS AV733872 cda Homo sapiens cDNA clone cdaASG06 5', mRNA sequence.

DEFINITION AV733872

ACCESSION AV733872

VERSION AV733872.1 GI:10851417

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919 (ex. 45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

1..618

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="cdaASG06"

/clone_1b="cda"

/tissue_type="pheochromocytoma"

/dev_stage="Adult"

/lab_host="BM25.8"

/note="Vector: pT7-1pEx2; Site_1: sfIIA; Site_2: sfIIB"

BASE COUNT 136 a 203 c 142 g 135 t 2 others

ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 618;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2050 TCGAAGCTCTGACCTGAGTATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAG 2109

Db 563 TCGAAGCTCTGACCTGAGTATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAG 504

OY 2110 G 2110

Db 503 G 503

Search completed: March 30, 2003, 19:49:22

Job time: 4114 secs